GenCore version 5.1.3 Coppright (c) 1993 - 2003 Compugen Ltd

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on:
                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq
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1: /SIDSZ/gcgdata/g
2: /SIDSZ/gcgdata/g
3: /SIDSZ/gcgdata/g
4: /SIDSZ/gcgdata/g
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                               100.0
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97.1
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-234-208B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988_DAT:*

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(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001_DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                                                                                                                                                                                                 Length
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            79
84
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79
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            ij
       AAE09196
AAE09185
AAE20349
AAE09188
AAE09199
AAE09199
AAE09191
AAE09184
AAE20350
AAE09192
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Human p68HER-2 ECD
Human p68HER-2 par
HER2 protein conta
Human p68HER-2 ECD
                                                                                                                                                                                                                                                            Description
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
86	86	ω	ω	ω	4	4	4	4	4	5	S	5	5	S	ū	ū	S	ū	S	S	Ç	υī	5	S	9	9	9	9	9	9	9	0	402	0
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459	459	419	419	419	419	419	79	419	419	419	419	420	419	419	419	419	419	419	419	79	79	79	419	419	419	79	79	79	79	79	79	79	79	79
20	20	22	22	22	22	22	22	22	22	22	22	21	23	22	22	22	22	22	22	23	22	21	22	22	22	22	22	22	22	22	22	22	22	22
ω	4	2	AAE09214	AAE09183	AAE09202	AAE09200	AAE09182	AAE09216	AAE09204	AAE09211	AAE09206	AAY97240	AAE20348	AAE09210	AAE09208	AAE09181	AAE09203	AAE09209	AAE09207	AAE20347	918	23	920	AAE09212	21		091		AAE09197	0919		091	0918	AAE09190 :
US recombin	US and CMP-	n p68HER-2	n p68HER-2	3HER-2	Human p68HER-2 gen	Human p68HER-2 gen	8HER-2	ပ်	8HER-2	ပ်	нER-2 ge	Truncated HER-2, p	truncated	2	p68HER-	p68HER-2	p68HER-2	N	Human p68HER-2 gen	HER2 intr	g	na	ပ်	2	p68HER-2	2	p68HER-2	p68HER-2	P68HER-2	p68HER-2	8HER-2 EC	8HER-2 EC	p68HER-2 EC	Human p68HER-2 ECD

ALIGNMENTS

RESULT 1

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AAE09196
ID AAEC
XX
 HER-2; herstatin; antagonist; extracellular domain; ECD; Herc
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                               Misc-difference
                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                           Human p68HER-2 ECDIIIa variant 11 encoded by HER-2 intron 8
                                                                                                                                                                                                                                                                                15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                       AAE09196;
                                                                                                                                                                                                                                                                                                                          AAE09196 standard; peptide; 79
(UYOR-) UNIV OREGON HEALTH SCI
                    16-FEB-2000; 2000US-0506079.
                                          16-FEB-2001;
                                                              23-AUG-2001
                                                                                    WO200161356-A1
                                                                                                                                                                                            Homo sapiens.
                                          2001WO-US05327
                                                                                                                                                            Location/Qualifiers
                                                                                                                               73
                                                                                                                                    /note= "p68HER-2 ECDIIIa (AAE09184)
                                                                                                        /note= "p68HER-2 ECDIIIa (AAE09184) Asp substituted with Asn which is encoded by CAC" ^{\prime\prime}
                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                   Pro
                                                                                                                                                   substituted
                                                                                                                                                                                                                                      Herceptin;
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AAE09185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised cantibody, Herceptin, at an affinity of at least 10°8. The present comment in the sased upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product cof the alternative transcript is a truncated HER-2 protein designated cof the alternative transcript is a truncated HER-2 protein designated cof the alternative transcript is a truncated HER-2 protein designated cof page 185 met. The present sequence and intracellular domains of the HER-2 receptor. The peptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify concleic acids encoding these are useful to treat, diagnose and identify coldidations. The present sequence is possessed by polymorphic form of human HER-2 intron 8.

CC (ANEROMAN) and the specification but is derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                               HER-2;
solid t
                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human p68HER-2 partial protein containing ECDIIIa variant sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE09185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE09185 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clinton
                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2001
                                                                                                                     Misc-difference
                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide, which binds treatment of hard tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGPDPDAHVAVNLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour;
                                                                                                                                                                                                                                                                                                                                                                          herstatin; antagonist; extracellular domain; ECD; Herceptin; tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ه</u>
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                                                                                                                                                                                                                                                                                                                                                         ECDIIIa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÃĄ;
                                                                  substituted with Leu"
  ECDIIIa
                                                                                                                                                                                                                                                         Location/Qualifiers
/note= "Asn is N-glycosylated. Most commonly occurring ECDIIIa (AAE09184) Asp substituted with Asn"
                                                                                          /note= "Most commonly occurring
                                                                                                                                         /note-
                                                                                                                                                                                       /note=
                                                                                                                                                                                                                /label=
                                                                                                                                           "Encoded
                                                                                                                                                                                       "Extracellular domain IIIA of p68HER-2"
                                                                                                                                                                                                                ECDIIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 418; DB 2
Pred. No. 2e-38;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                          ECDIIIa (AAE09184) Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
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B ş Вb QΥ

/note=

"Encoded by GGCTGAGACGGCCCCTTCCCCCACCCACCCCACC

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RESULT 3
AAE20349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 partial protein containing ECDIIIa variant sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different of the binding site of humanised antibody, Herceptin, at an affinity of at least 10'8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product
                                                                                                                                                  Endothelial growth factor receptor; EGFR; HER-2 receptor tyrosine kinase: emmanor:
                                                                                                                                                                                                                                                                            AAE20349 standard; Protein; 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-529934/58.
N-PSDB; AAD15854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200161356-A1
           Misc-difference
                                                                                                                                     glial
                                                                                                                                                                                          HER2 protein
                                                                                                                                                                                                                     18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2001; 2001WO-US05327
                                     Modified-site
                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, which binds to the extracellular domain of \ensuremath{\mathsf{HER-2}} for treatment of hard tumors -
                                                                                                                                                                                                                                                                                                                                                             GRGPDPDAHVAVNLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                GRGPDPDAHVAVNLSRYEG
                                                                                                                                   receptor tyrosine kinase; cell tumour; cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Henner WD,
                                                                                                                                                                                          containing
                                                                                                                                                                                                                     (first entry)
                                                              Location/Qualifiers
                                     /note=
75..77
        /note= "Asn is N-glycosylated" 81..82
                                                 "Encoded by CCCGA"
                                                                                                                                                                                          extracellular domain (ECDIIIa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evans A;
                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 418; DB 22;
Pred. No. 2.1e-38;
                                                                                                                                                                                                                                                                              AA
                                                                                                                                                tor; EGFR; tumour; cytostatic; l
squamous cell carcinoma; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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В
                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for treating a solid tumour characterised by endothelial growth factor receptor (EGFR) expression. The method involves administering an agent that binds to an extracellular domain (ECD) of EGFR. The invention also relates to a naturally occurring inhibitor of HER-2 receptor tyrosine kinase called herstatin. The coexpression of herstatin with pl85HER2 causes a striking reduction in cell growth that corresponds with suppression of pl85 autophosphorylation. The method or a pharmaceutical composition is useful for treating a solid tumour (selected from squamous cell carcinoma, lung carcinoma, colon carcinoma and glial cell tumour) characterised by EGFR expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating solid tumor characterized by expression of endothelial growth factor receptor, involves administering recombinant herstatin that binds to extracellular domain of the endothelial growth factor receptor
               Misc-difference
                                                     Homo
                                                                           P68HER-2;
                                                                                        HER-2; herstatin;
solid tumour; canc
                                                                                                     HER-2;
                                                                                                                          Human p68HER-2 ECDIIIa variant 3 encoded by HER-2 intron
                                                                                                                                                     15-NOV-2001
                                                                                                                                                                              AAE09188,
                                                                                                                                                                                                    AAE09188 standard; peptide; 79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is HER2 protein containing extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-269185/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Fig 1; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200214470-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          (ECDIIIa)
                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                               GRGPDPDAHVAVNLSRYEG
                                                    sapiens
                                                                                                                                                                                                                                                                 GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD32539
                                                                            ECDIIIa; variant
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   84 AA;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0638834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US25502
                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCAGTG"
9 83..84
               Location/Qualifiers
   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by
                                                                                     antagonist; extracellular domain;
cer; polymorphism; cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                             100.0%;
"p68HER-2 ECDIIIa (AAE09184) Pro substituted
                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                               Score 418; DB 23; Pred. No. 2.1e-38; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCT'
                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                  ECD;
                                                                                    therapy;
                                                                                                 Herceptin;
                                                                                                                                                                                                                                                                                                                                                                                         84;
                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 5
AAE09195
ID AAE0
 В
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                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC uncleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 ECDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 CC (AAF09194).
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                         AAE09195 standard; peptide;
                                           Homo sapiens
                                                                          P68HER-2;
                                                                                      HER-2; herstatin; antagonist; extracellular domain;
solid tumour; cancer; polymorphism; cytostatic; gene
                                                                                                                                  Human p68HER-2 ECDIIIa variant 10
                                                                                                                                                               15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AAE09184).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11; Page -; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200161356-A1
                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, which binds to the extracellular domain of HER-2 for treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                                         GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV
                                                                                                                                                                                                                                                                                                                                                           GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV
                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIV OREGON HEALTH
                                                                          ECDIIIa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                        cancer; polymorphism;
[IIa; variant.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                  98.8%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans A;
                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 413; DB 2
Pred. No. 7e-38;
1; Mismatches
                                                                                                                                                                                                                            Ą
                                                                                                                                  encoded by HER-2 intron
                                                                                      cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                    ECD; Herceptin;
                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                           60
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0;

Misc-difference

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RESULT 6
AAE09199
В
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                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is p68HER-2 ECDIIIa variant encoded by polymorphic form of human HER-2 intron 8.

Note: The present sequence is not shown in the specification but is derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10'8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clinton G, Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2001; 2001WO-US05327
                             Homo sapiens.
                                                           HER-2; herstatin; antagonis solid tumour; cancer; polymp68HER-2; ECDIIIa; variant.
                                                                                                                         Human p68HER-2
                                                                                                                                                         15-NOV-2001
                                                                                                                                                                                          AAE09199
                                                                                                                                                                                                                      AAE09199 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide, which binds to the extracellular domain of \ensuremath{\mathsf{HER-2}} the treatment of hard tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200161356-A1
                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                    GRGPDPDAHVAVNLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                                                 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                  GTHSLPPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-529934/58
DB; AAD15864.
                                                                                                                                                                                                                                                                                                     GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
78; Conserver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0506079.
                                                                           cancer; polymorphism; cytostatic;
                                                                                                                           ECDIIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "p68HER-2 ECDIIIa (AAE09184) Asp substituted
with Asn which is encoded by CAC"
                                                                                          antagonist; extracellular domain; ECD; Herceptin;
                                                                                                                                                                                                                                                                                                                                                                                                                                            98.3%;
                                                                                                                        variant 15 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans A;
                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 411; DB 22;
Pred. No. 1.2e-37;
0; Mismatches 1;
                                                                                                                                                                                                                       ΑĀ
                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 79
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                           therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
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Кеу

Location/Qualifiers

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RESULT 7
AAY97241
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                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC uncleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 EDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 CC (ABERGIA)
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-2000; 2000US-0506079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 73
                                        HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion; extracellular domain IIIa; antagonist; intron 8; C-terminal extension; truncated HER-2; p68; dimerization inhibitor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD15868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2001; 2001WO-US05327
                                                                                                       HER-2 C-terminal extracellular domain
                                                                                                                                      04-DEC-2000 (first entry)
                                                                                                                                                                                                  AAY97241 standard; Protein; 79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2001
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                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                          ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, which binds to treatment of hard tumors -
                                                                                                                                                                                                                                                                                               GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                           GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                               GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                        78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page -; 6lpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "p68HER-2 ECDIIIa (AAE09184) Asp substituted with Asn" \,
                                                                                                                                                                                                                                                                                                                                                                                                                     98.3%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans A;
                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 411; DB 22;
Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the extracellular domain of HER-2
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                      IIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                            60
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RESULT 8
AAE09184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. The extracellular domain of p185-HER-2 is proteolytically shed from breast carcinoma cells in culture and is found in serum of some cancer patients and may be a serum marker of metastatic breast cancer. An alternative HER-2 mRNA of 4.8 kb with a 274 bp insert (intron 8) has been dentified. The retained intron is in-frame and encodes a 79 amino acid extension designated ECDIIIa (the present sequence), which is inserted at residue 340 of p185-HER-2. The alternative mRNA predicts a truncated HER-2 protein (approximately 68 kba) that lacks the transmembrane and intracellular domains (see AAY97240), p68HER-2 specifically binds to p185-HER-2 without activating HER-2. It could therefore block dimerization of p185-HER-2. The p68HER-2 polypeptide binds to a site on the ECD of HER-2 that is different from the site of binding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herceptin (RTM) (a marketed humanized monoclonal antibody that is used for the treatment of cancer and binds to the ECD of HER-2). The methods, compositions, polypeptides and antibodies are used to treat solid tumours such as breast cancer, small cell lung carcinoma, ovarian cancer and/or colon cancer, especially where over-expression of HER-2 is
                              Homo sapiens
                                                                                 HER-2; herstatin;
solid tumour; can
                                                                                                                              Human p68HER-2 ECDIIIa domain encoded by HER-2 intron 8.
                                                                                                                                                                 15-NOV-2001
                                                                                                                                                                                                                               AAE09184 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-499287/44.
N-PSDB; AAA53783.
                                                              p68HER-2; ECDIIIa; intron 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Page 42-43; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breast, lung, ovaries and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Using polypeptides and antibodies that bind to the extracellular domain of the receptor-like tyrosine kinase HER-2 to treat solid tumors of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYOR-) UNIV OREGON HEALTH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200044403-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-2000; 2000WO-US01484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               indicated
                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                                                        1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                          GRGPDPDAHVAVNLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                                                        GTHSLPPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                      GRGPDPDAHVAVDLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clinton GM,
                                                                              tin; antagonist; extracellular domain; ECD; Herceptin;
cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0234208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adelman
                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 406; DB 21;
Pred. No. 4.1e-37;
                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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AAE20350
Вр
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIa. The ECDIIIA-contains ECD I, II of the p185HER-2 and the novel ECDIIIA the ECDIIIA-contains polypeptides bind tiphtly to, and thus anragonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is ECDIIIa domain of human p68HER-2 protein encoded by intron 8 of HER-2 gene.
                                                                                                                                                nerstatin; HER-2 receptor tyrosine kinase; colon; glial cell tumour; cell growth.
                                                                                                                                                                                                                                                                                                         AAE20350 standard; Protein;
             14-AUG-2000; 2000US-0638834
                                                                                                  WO200214470-A2
                                                                                                                            Homo sapiens
                                                                                                                                                                       Human; tumour; endothelial growth factor receptor; EGFR;
herstatin; HER-2 receptor tyrosine kinase; squamous cell
                                                                                                                                                                                                                   Human HER2 intron 8 encoded protein.
                                                                                                                                                                                                                                              18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                           AAE20350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD15853, AAD15869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clinton G,
                                         14-AUG-2001; 2001WO-US25502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Fig 8; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYOR-) UNIV OREGON HEALTH SCI
                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide, which binds to treatment of hard tumors -
                                                                                                                                                                                                                                                                                                                                                                               GRGPDPDAHVAVDLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                                                                           GRGPDPDAHVAVNLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US05327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.1%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans
                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 406; DB 22;
Pred. No. 4.1e-37;
                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the extracellular domain of HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                        cytostatic;
carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                     lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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RESULT 10
AAAE091.92
ID AAE09
XX AAE09
AC AAE09
XX AE09
XX HER-
KW HER-
KW Soli
KW P68F
XX P68F
XX HOMC
XX HOMC
XX HOMC
XX P1 Mis
FT Mis
FT Mis
PD 23
XX PF 16
XX PF 16
XX PF 16
XX PR 16
XX PA (1
XX PA (1
XX PA (1
XX PA (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for treating a solid tumour characterised by endothelial growth factor receptor (EGFR) expression. The method involves administering an agent that binds to an extracellular domain (ECD) of EGFR. The invention also relates to a naturally occurring inhibitor of HER-2 receptor tyrosine kinase called herstatin. The coexpression of herstatin with pl85HER2 causes a striking reduction in cell growth that corresponds with suppression of pl85 autophosphorylation. The method or a pharmaceutical composition is useful for treating a solid tumour (selected from squamous cell carcinoma, lung carcinoma, colon carcinoma and glial cell tumour) characterised by EGFR expression. The present sequence is a protein encoded by human HER2 intron 8.
    Clinton G,
                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                          HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAE09192;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE09192 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating solid tumor characterized by expression of endothelial growth factor receptor, involves administering recombinant herstatin that binds to extracellular domain of the endothelial growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-269185/31.
N-PSDB; AAD32540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clinton
                                 (UYOR-) UNIV OREGON HEALTH SCI.
                                                               16-FEB-2000;
                                                                                            16-FEB-2001;
                                                                                                                                                        WO200161356-A1
                                                                                                                                                                                                                                                                                                                                                    Human p68HER-2 ECDIIIa variant 7 encoded by
                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYOR-) UNIV OREGON HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 11; Fig 8; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GRGPDPDAHVAVDLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 AA;
    Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                               2000US-0506079.
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                            2001WO-US05327
                                                                                                                                                                                     /note= "p68HER-2 ECDIIIa (AAE09184) Leu substituted with Ile"
                                                                                                                                                                                                                   Location/Qualifiers 36
                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.1%;
97.5%;
    Evans A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 406; DB 23;
Pred. No. 4.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                       HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 11
AAE09190
ID AAE09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the novel ECDIII a coids encoding these are useful to treat, diagnose and identify C solid tumours. The present sequence is p68HER-2 ECDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC Note: The present sequence is not shown in the specification but is CC (AAEO1914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-529934/58
N-PSDB; AAD15861.
                                                                                                                                                                                                                                                                                                                                                                              AAE09190;
                                                                                                                                                                                                                                                                                                                                                                                                        AAE09190 standard; peptide; 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide, which binds the treatment of hard tumors
                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                              p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                         HER-2; herstatin; antagonist; extracellular solid tumour; cancer; polymorphism; cytostat
                                                                                                                                                                                                                                                                                                                     Human p68HER-2 ECDIIIa variant 5 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Page -; 61pp; English.
                                       16-FEB-2000; 2000US-0506079.
                                                                    16-FEB-2001;
                                                                                                                             WO200161356-A1
                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AAE09184).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>_</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                    2001WO-US05327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                     Location/Qualifiers 18
                                                                                                                                                       /note= "p68HER-2 ECDIIIa (AAE09184) Met with Leu which is encoded by ATA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 404; DB 22;
Pred. No. 6.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                          cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular domain of HER-2
                                                                                                                                                                                                                                                                                           domain;
                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                           ECD;
                                                                                                                                                                                                                                                                         therapy
                                                                                                                                                                        substituted
                                                                                                                                                                                                                                                                                        Herceptin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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(UYOR-) UNIV OREGON HEALTH SCI

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RESULT 12
AAE09186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        particularly a polypeptide that binds to the extracellular domain (ECD) Cof HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10-8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of The HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is p68HER-2 ECDIII variant cencoded by polymorphic form of human HER-2 intron 8.

Note: The present sequence is not shown in the specification but is derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                             HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2; ECDIIIa; variant.
                             16-FEB-2000; 2000US-0506079
                                                                                                                         WO200161356-A1
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                           Human p68HER-2
                                                                                                                                                                                                                                                                                                                                                        15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09186 standard; peptide; 79
(UYOR-) UNIV OREGON HEALTH SCI
                                                           16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide, which binds to the extracellular domain of HER-2 for the treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRGPDPDAHVAVDLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÃĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to novel HER-2
                                                                                                                                                                                                                                                                                                                       ECDIIIa variant 1 encoded by HER-2 intron
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                      /note= "p68HER-2 ECDIIIa (AAE09184) Thr substituted with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 403; DB 22;
Pred. No. 8.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (herstatin-2) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 13
AAE09189
Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  particularly a polypeptide that binds to the extracellular domain (ECD) cof HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p69HER-2 which lacks the transmembrane and intracellular domains of 20°C p185HER-2 but contains ECD I. II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides bind tightly to, and the novel ECDIIIa concleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is p68HER-2 ECD, and the concleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is p68HER-2 ECDIIIa variant are necessary to the present sequence is not shown in the specification but is concleic acids encoded by polymorphic form of human HER-2 intron 8 encoded ECDIIIa sequence given in figure 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                           Location/Qualifiers
              16-FEB-2000; 2000US-0506079
                                               16-FEB-2001; 2001WO-US05327.
                                                                                                                                                                                                                                                                                             HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                    WO200161356-A1
                                                                                                                                                                                                                                                                           p68HER-2; ECDIIIa;
                                                                                                                                                                                                                                                                                                                                               Human p68HER-2 ECDIIIa variant 4 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      AAE09189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE09189 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide, which binds to the extracellular domain of HER-2 the treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRGPDPDAHVAVDLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSHSLPPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                   /note= "p68HER-2 ECDITIa (AAE09184) Leu substituted with Gln"
                                                                                                                                                                                                                                                                               variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.2%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 402; DB 22;
Pred. No. 1.1e-36;
2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                            gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 14
AAE09187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p189HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA contains pCD I, II of the p185HER-2 and the novel ECDIIIa contains pclypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC nucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 intron 8.

CC Note: The present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is fixed to the contains of the present sequence is not shown in the specification but is the contains of the present sequence is not shown the contains of the present sequence is not shown the contain
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Best Local S
Matches 76
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                                          16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                             HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human p68HER-2 ECDIIIa variant 2 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE09187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE09187 standard; peptide; 79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYOR-) UNIV OREGON HEALTH
16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                             p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived from
                                                                                         23-AUG-2001
                                                                                                                                      WO200161356-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide, which binds to the extracellular domain of \ensuremath{\mathsf{HER-2}} treatment of hard tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-529934/58
                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HER-2 intron 8 encoded ECDIIIa sequence given in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                 /note= "p68HER-2 ECDIIIa (AAE09184) Leu substituted
with Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.7%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 400; DB 22;
Pred. No. 1.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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RESULT 15
AAE09191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC pf8HER-2 which lacks the transmembrane and intracellular domains of CC pf8HER-2 but contains ECD I, II of the pf85HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC uncleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 ECDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC Note: The present sequence is not shown in the specification but is CC (Arengalaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                               15-NOV-2001
                                                                                                                                                                                                                                                                                                                            AAE09191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Page -; 61pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide, which binds the treatment of hard tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD15856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-529934/58
                                                                                                                                                                                                                       HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                Human p68HER-2 ECDIIIa variant 6 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                       AAE09191 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYOR-) UNIV OREGON HEALTH SCI
                                                                      WO200161356-A1
                                                                                                                                 Misc-difference
                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                GRGPDPDAHVAVDLSRYEG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
76; Conser
                                                                                                                                                                                                      our; cancer; polymorphism; cytostatic;
ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
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                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑA;
                                                                                                                               Location/Qualifiers
                                                                                                /note= "p68HER-2 ECDIIIa (AAE09184) Gly substituted
with Asp, Ala or Val"
                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.5%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 399; DB 22;
Pred. No. 2.4e-36;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular domain
                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                     therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of HER-2 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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16-FEB-2001; 2001WO-US05327

23-AUG-2001.

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                                                                                                                                                           Вb
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                                                                                                                                                                                                                                                                                                                      The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC nucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 ECDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8. CC derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 carived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8.
                                                                                                                                                                                                                                     Query Match 95.5
Best Local Similarity 96.2
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clinton G, Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide, which binds to the extracellular domain of HER-2 for the treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD15860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-2000; 2000US-0506079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Page -; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                            (AAE09184).
                                                                          1
                                                                                                                                                                           1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                         GTHSLPPRPAAVPVPLRMQPXPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                    79 AA;
                                                                                                                                                                                                                                                        95.5%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans A;
                                                                                                                                                                                                                                   Score 399; DB 22;
Pred. No. 2.4e-36;
1; Mismatches 2;
                                                                                                                                                                                                                                                                           Length 79;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                   0;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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Copyright (c) 1993 - 2003 Compugen Ltd
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S39161
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ALIGNMENTS

C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000

R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, J. Biol. Chem. 267, 19536-19547, 1992

R.U.; Margolis, R.K.

C; Accession: S28764

neurocan precursor - rat

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1257 < RAU'>
A; Cross-references: EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g205650
C; Superfamily: aggrecan; C-type lectin homology; complement factor H repeat
C; Keywords: chondroitin sulfate proteoglycan; glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1257/Product: neurocan #status predicted <MAT'>
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
                                                                                                                                         probable phytocyanin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84715
                        R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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F;953-984/Domain: EGF homology <EGF>
F;1029-1149/Domain: C-type lectin homology <LCH>
F;1156-1212/Domain: complement factor H repeat homology <FHD>
F;1121.339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status profits F;372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental
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A;Title: Cloning and primary structure of neurocan, a developmentally regulated, A;Reference number: S28764; MUID:92406907; PMID:1326557
A;Accession: S28764
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Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
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35.0%;
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DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - Arabidopsis thaliana N,Alternate names: DNA-directed RNA polymerase II 205K chain; protein F4B14.70 C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 31-Mar-1993 #sequence_revision II-Jun-1999 #text_change 20-Aug-1999 C:Accession: T04690; S12071; S27346; S11960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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A;Gene: At2g31050
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A; Residues: 1-200 <STO>
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A; Accession: H84715
A; Status: preliminary
A; Accession: T04690
A; Molecule type: DNA
                                                          R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; submitted to the Protein Sequence Database, October 1998
                                                                                  C;Accession:
R;Bevan, M.;
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A; Residues: 1-1006 <STO>
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                                         A; Reference number: 215380
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                                                                                                   A; Map position:
C; Superfamily: }
                                                                                                                                            A; Gene:
                                                                                                                                                                    C; Genetics
                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                       A; Molecule type: DN
A; Residues: 1-1840
                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                   A; Title: Sequence and analysis of A; Reference number: A85001; MUID: A; Accession: G85422
                                                                                                                                                                                                                                                                                                                                  R; anonymous, The Eur
Nature 402, 769-777,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G85422
                                      Best
                     Matches
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: AT4g35800 position: 4

DNA-directed 19.1%; 36.4%;

RNA polymerase

II largest

DNA

<STO>
: GB:NC_001268;

NID: g7270532; PIDN: CAB81489.1;

GSPDB:GN00140

The European Union Arabidopsis Genome Sequencing Consortium, The Cold 169-777, 1999

#text_change 02-Mar-2001

sis of chromosome 4 of the plant Arabidopsis thaliana MUID:20083488; PMID:10617198

Local Similarity es 28; Conserv

Conservative

Pred. No. 7.7 3; Mismatches

36;

10;

ω

Score 80;

DB 2; 7.7;

Length 1840; Indels

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A:Introns: 28/3; 123/3; 218/3; 271/3; 325/3; 411/
A:Note: F4B14.70
C:Superfamily: human DNA-directed RNA polymerase
C:Keywords: DNA binding; nucleotidyltransferase;
F:66-109/Region: zinc finger CCCC motif
F;1531-1812/Region: 7-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-116,125-192, 'NSKEE',198-297,'R',299-302,'R',304-400,'KE',403,'VDYGPHPPP
A;Cross-references: EMBL:X52494; NID:g16493; PIDN:CAA36735.1; PID:g16494
A;Note: the authors translated the codon CCT for residue 1083 as Ala
C;Genetics:
C;Genetics:
A;Gene: rpII215; RPB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: cv. Columbia
R;Dietrich, M.A.; Prenger, J.P.; Guilfoyle, T.J.
Plant Mol. Biol. 15, 207-223, 1990
A;Title: Analysis of the genes encoding the largest subunit of RNA polymerase II in A A;Reference number: S11960; MUID:91355869; PMID:2103447
A;Accession: S11960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: cultivar Columbia; R; Nawrath, C.; Schell, J.; Koncz, C. Mol. Gen. Genet. 223, 65-75, 1990
hypothetical protein AT4g35800 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: G85422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 510-732,'D',734-1055,'R',1057-1714,'SPTSPSY',1715-1834 <NAW2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the authors translated the codon AGC for residue 1755 A;Accession: $27346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-421, 'S', 423-732, 'D', 734-1055, 'R', 1057-1714, 'SpTSpSy', 1715-1834 A; Cross-references: EMBL: X52954; NID: g16504; PIDN: CAA37130.1; PID: g16505 A; Experimental source: cv. Columbia
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Best Local
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Pred. No. 7.6;
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A; Status, Free DNA
A; Molecule type: DNA
A; Residues: 1-217 <SCH>
A; Cross-references: EMBL: AL389900; GSPDB: GN00116; NCSP:B15120.10
A; Cross-imantal source: BAC clone B15120; strain OR74A
                                                                                                                                                                                                                                                           A; Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related to finger protein XFG 68 [imported] - Neurospora crassa N;Alternate names: protein B15I20.10 C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: T51031 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S72619
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-249 <HEA>
A; Cross references: EMBL:L76172
A; Cross references: EMBL:T6172
A; Note: in the authors' translation residues 1-10 are not shown C; Genetics:
C; Genetics:
A; Mobile element: retrotransposon CgTl
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A;Title: CgTl: a non-LTR retrotransposon with restricted distribution A;Reference number: S72619; MUID:96439839; PMID:8842152
A;Accession: S72619
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C;Accession: S72619
R;He, C: Nourse, J.P.; Kelemu, S.; Irwin, J.A.G.; Manners, J.M.
                                                                                                                                        80
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A; Accession: T51031
hypothetical
                      T19319
                                         RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVPRWVCHPNTNTAQPTPQRQEPSPAMASQPAAGPSQGPIGLLSSMHNLPKTPPPPTSLP 83
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                                                                                                                                                                                 21;
protein C15H11.5
                                                                                                                                                                                                 Similarity
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Sequence Database,
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    ,
Caenorhabditis elegans
                                                                                                                                                                           Score 77.5; DI
Pred. No. 1.2;
5; Mismatches
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                                                                                                PS---TSALVLLPVSPLPSSSSPLIPCSPRR 155
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1.2;
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2010
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S
                                                                                                                                                                                     C:Accession: A96826
C:Accession: A96826
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alc
                                                                                                                                                                                                                                                                                                                                  T8K14.10 [imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
A96826
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A;Residues: 1-1110 <WIL>
A;Cross-references: EMBL:Z48367; PIDN:CAA88324.1; GSPDB:GN00020; CESP:C33B4.3
A;Experimental source: clone C33B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19673
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19319
R;Bardill, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2
A; Introns: 20/3; 110/3; 144/3; 341/1; 455/1; 546/1; 653/3; 934/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from A;Molecule type: DNA
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A; Accession: T19673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-503 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 32.7 Local Similarity 32.7 Local Similarity
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24; Conser
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Pred. No. 9.6;
L2; Mismatches
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Pred. No.
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                                                                           Maiti,
                                                                                                                 Khaykin,
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                                                                               Marzia
                                                                                                                     Kim,
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Southwick, A.M.; Sun, H.; Tallo

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C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002 C;Accession: S48273; S45976; S44688 R:Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 10, 1363-1381, 1994 A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II. A;Reference number: S48255; MUID:95208357; PMID:7900426
genome-linked protein VPg - soybean dwarf virus
C:Species: soybean dwarf virus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C:Accession: D49600
R:Rathjen, J.P.; Karageorgos, L.E.; Habili, N.; Waterhouse, P.M.; Symons, R. Virology 198, 671-679, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: $45976
A; Accession: $45976
A; Molecule type: DNA
^.Posidues: 1-848 <FE2>
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A;Molecule type: DNA
A;Residues: 1-356 <STO>
                                                                                                                        RESULT
D49600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable transcription factor YBR108w -
N;Alternate names: hypothetical protein
C;Species: Saccharomyces cerevisiae
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: A96826
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A; Map position:
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                                                                                                                                                                                                       LPPPPTH 449
                                                                                                                                                                                                                                                                                    PVPVRMQPQPPQPMQQGNIYPIEPSLDSTGSTPHFEVTPFDPDAPAPKPKIDIPTVDVSS 442
                                                                                                                                                                                                                                                                                                                         PVPLRMQPGPAHPV----LSFLRPSWDLVSA---FYSLPLAPLSPTSVP---ISPVSVGR 62
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23; Conser
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                      P.M.; Symons, R.H
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A;Status, France, A;Status, France, DNA
A;Nolecule type: DNA
A;Residues: 1-1952 <SCH>
A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220
A;Cross-importal source: cosmid contig 15E6; Strain 74
                                                  A;Notecule type: DNA
A;Nolecule type: DNA
A;Residues: 1-894 <BEV>
A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.170
A;Cross-references: cultivar Columbia; BAC clone F8L21
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A; Accession: T48814
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C;Speciles: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-M
C;Accession: T48814
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A; Residues: 1-189 < RAT>
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                                                A; Experimental source: cultivar C; Genetics:
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A; Introns: 281/3
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               A;Gene: ATSP:F8L21.170
A;Map position: 4
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C; Superfamily: beta-adaptin

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hypothetical protein KIAA0595 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00273
R;Nagase, T; IShikawa, K; Miyajima, N; Tanaka, A; Kotani, H; Nomura, N; Ohara, O. DNA Res. S, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A;Reference number: 214086; MUID:98290545; PMID:9628581
A;Accession: T00273
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type; mRNA
A;Residues: 1-1520 <NAG>
A;Cross-references: EMBL:AB011167; NID:g3043713; PIDN:BAA25521.1; PID:g3043714
A;Experimental source: brain
C;Genetics:
A;Note: KIAA0595
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** AB022433; BAB206 ** AF216389; AAF876 ** HGNC:10739; SEW ** FPro; IPR003659; F ** Pro; IPR007627; S ** PFO1403; Sema; I **; SM00283; PSI; I **; SM00283; PSI; I **; SM00286; PTI; SM00286; PTI; I **; SM00286; PTI; SM00286; PTI; I **; SM00286; PTI; SM00286; PTI; I **; SM0	PROT e ne Swis nn Bioi nn-prof nd this guires email	Human semaphorin 6b."; Human semaphorin 6b."; Human semaphorin 73:343-348(20) - FUNCTION: MAY PLAY SYSTEM DEVELOPMENT - SUBCELLULAR LOCATIO - ALTERNATIVE PRODUCT 2/6B.1; are produce - SIMILARITY: BELONGS - SIMILARITY: CONTAIN	ROM N.A 248680; ., Sasa 1., Bre	M N.A ; shida an-19	SEMAZ. SEMAZ. Human Metazoa; Sutheria; 9606;	16-OCT-2001 (Rel. 40 16-OCT-2001 (Rel. 40 15-JUN-2002 (Rel. 41 Semaphorin 6B precur:	ST		115.9 15.9 15.8 15.8
AB20669.1; AF87661.1; AF87661.1; AF87661.1; SEMAGB. 59; Plexin 27; Sema. 37; Squash na; 1. 171	ntry is s Insti s Insti informat it ins statem a lice to lice	AND THE PRODUCTS: IVE PRODUCTS: IV	N.A. (ISOFORM 680; PubMed=113 Sasahara R.M., Brentani M.M.,	. (ISOF H.; 99) to	Choi Prin	ς, , , , , , , , , , , , , , , , , , ,	ANDARD;		360 817 1433 259 283 322 435 1229 558 736 868
7669.1; 7661.1; 2MA6B. Plexin- Sema. Squash. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	cop tute ics titu ent ent ense nse	O1). A ROLE A ROLE OF SIN ON: Type of Sin On Type)FORM ed=113 e.m., m.m.,	SOFORM to the	data	eate			
family; Neurogenes re splicing. NTIAL. APHORIN 6B.	t is produced formatics an formatics an There are long as its moved. Usage (See http://h).	rin 6b."; 3-348(2001). 3-348(2001). MAY PLAY A ROLE IN BOTH PERIPHERAL AND ELOPMENT (BY SIMILARITY). R LOCATION: Type I membrane protein. E PRODUCTS: At least 2 isoforms; 1 (she produced by alternative splicing. BELONGS TO THE SEMAPHORIN FAMILY. CONTAINS 1 SEMA DOMAIN.	2). 350127; Bengtson M.H., Katayama , Sogayar M.C., de Souza	1). EMBL/GenBank/DDBJ databas	Craniata; Verteb	reated) st sequence update) st annotation update) (Semaphorin Z) (Sema Z)	PRT; 888 AA.	ALIGNMENTS	A2HS_RABIT VRP1_YEAST Y310_HUMAN MSP8_EIMAC EXYN_SORBI RX1_XENLA TEA3_HUMAN M121_HUMAN TTEA5_CHICK ORP9_HUMAN DCC_HUMAN
; Glycop	d through a collaboration and the EMBL outstation on restrictions on it content is in no was e by and for commercial /www.isb-sib.ch/announce,	D CENTRAL NERVOUS	M.L.H.,	ଭି ଓ ଓ ଓ .	<pre>Euteleostomi; ; Homo.</pre>				P80191 oryctolagus p37370 saccharomyc o15027 homo sapien p09125 eimeria ace p24152 sorghum bic o42201 xenopus lae o99594 homo sapien p98152 gallus gall Q96su4 homo sapien o35569 rattus norv p43146 homo sapien

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RESULT 2
PGCN_RAT
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Best Local S
Matches 28
                                                                   Margolis R.U., Grumet M.;

"The neuronal chondroitin sulfate proteoglycan neural cell adhesion molecules Ng-CAM/LL/NILE a neuronal adhesion and neurite outgrowth.";

J. Cell Biol. 125:669-680(1994).

-i- FUNCTION: MAY MODULATE NEURONAL ADHESION AND N-CAM). CHONDROITIN SULFATE PROTEOGLYCA
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p1-007-1996 (Rel. 34, Created)

01-007-1996 (Rel. 34, Last sequence update)

16-007-2001 (Rel. 40, Last annotation update)

Neurocan core protein precursor (245 kDa early postnatal configuration) [Contains: 150 kDa adult core glycoprotein].
                                                                                                                                                                 MEDLINE-94230574;
                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                              Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.; "Cloning and primary structure of neurocan, a developmentally regulated, aggregating chondroitin sulfate proteoglycan of brain."; J. Biol. Chem. 267:19536-19547(1992).
                                                                                                                                                      Friedlander D.R., Milev
                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-92406907; PubMed-1326557;
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NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                      CSPG3 OR NCAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEN
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    869
                                                                                                                                                                                                                                                                                                                                                                                                                                              757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
                                            ACID.
TISSUE SPECIFICITY: EARLY POSTNATAL
                     IN KIDNEY, LUNG, LIVER AND MUSCLE.
PTM: CONTAINS MOSTLY CHONDROITIN SULFATE,
O-LINKED OLIGOSACCHARIDES (BY SIMILARITY)
   PTM: TWO ISOFORMS DEGRADATION. THE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              RAPEQPPAPGE-PTPDGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPISPVSVGRGPDPDAHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPHDLDSGLLPTPEQTPLPQKRLPTP-HPHPHALGPRAWDHGHPLLPASASSSLLLLAPA 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604
625
638
661
750
750
74
155
167
167
291
386
441
441
                                                                                                                                           Grumet M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                 PubMed=7513709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888
30
95270
                                                                                                                                                                                                                                                          AND
                                                                                                                                                                                                                                                                                        Rodentia;
                                                                                                                                                                                                                                                                                                   Chordata;
   LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.0%;
WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL
                                                                                                                                                                                                                                                          PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. v.o.
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAFPRC -> RVCQVGHACRVCVHERRSWWPQRPGRWLSRR WGFQKARGPPRCRLGV (IN ISOFORM 1).
MISSING (IN ISOFORM 2).
D -> E (IN REF. 2).
; 6FFB44D6828C70CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSVFLEEFETYRPDRCGRPGGGETGQRLLSLELDAASGGLL
                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.5;
No. 0
                                                                      ADHESION AND NEURITE GROWTH DURING L CELL ADHESION MOLECULES (NG-CAM PROTEOGLYCAN; BINDS TO HYALURONIC
                                                                                                                                                                                                                                                                                                                                                                                          1257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
                                                                                                                                                   L.,
                                                  AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                      Margolis R.K.,
                                                  ADULT
                                                                                                                                                                                                                                                                                        Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                        n neurocan k
and N-CAM,
                              BUT ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .) (POTENTIAL).
. .) (POTENTIAL).
. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 888;
                                                    BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                       Euteleostomi;
; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                     SIGNAL
CHAIN
                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                         Glycoprotein;
EGF-like doma:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M97161;
                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00008;
PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00059;
  58
181
205
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279
303
958
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1029
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1185
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274
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SMART; SM00032; CCP; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00179; EGF_CA; 1.

SMART; SM00010; EGF_L1ke; 1.

SMART; SM000409; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM000409; IG; 1.

SMART; SM00010; ASX_HYDROX
PROSITE; PS001002; EGF_1; 3.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01147; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00193; Xlink; 2. ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 LINK DOMAINS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IPR003599; Ig.
; IPR003006; Ig_MHC.
; IPR003004; Lectin_C.
; IPR000538; Link.
; IPR000436; Sushi_SCR_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001881;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                041; C_TYPE_LECTIN_2; 1.
Hyaluronic acid; Proteoglycan; Immunoglobulin
hyaluronic acid; Lectin; Sushi; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC37679.1; -.
1EDM.
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Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASX_HYDROXYL; 1.
EGF_1; 3.
EGF_2; 1.
EGF_CA; 1.
LINK; 2.
C_TYPE_LECTIN_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L52; Asx_hydroxyl.
    institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF_2.
EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like
150 KDA ADULT OF TYPE
LINK 1.
LINK 2.
EGF-LIKE 2. CAL
EGF-LIKE 2. CAL
C-TYPE LECTIN.
SUSHI.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEUROCAN CORE PROTEIN.
150 KDA ADULT CORE GLYCOPROTEIN
IG-LIKE V-TYPE DOMAIN.
    (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ng as its content is in
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                         (POTENTIAL)
    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
 ProDom; PD000425; TF_Fork_head; SMART; SM00339; FH; 1.
PROSITE; PS00657; FORK_HEAD_1; 1
PROSITE; PS00658; FORK_HEAD_2; 1
PROSITE; PS50039; FORK_HEAD_3; 1
                                                                                                                                 EMBL; X92591; CAA63335.1;
EMBL; X71942; CAA50744.1;
HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q64733;
01-NOV-1997
                                                                             TRANSFAC; T02442; -.
MGD; MGI:1347468; Foxb2.
InterPro; IPR001766; TE_Fork_head.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression of the winged helix genes fkh-4 and fkh-5 defines domains in the central nervous system.";
Mech. Dev. 55:221-230(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=97014266; PubMed=8861101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOXB2 OR FKH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forkhead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FXB2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                         Proc. Nati.
                                                                                                                                                                                                                                                                                                                                                   regulated.";
                                                                                                                                                                                                                                                                                                                                                                             Kaestner K.H., Lee K.H., S
Monaghan A.P., Schuetz G.;
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93361500; PubMed=7689224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                  "Six members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SLLPRPAAVPVPLRMQPG---PAHPVLSFLR-----PSWDLVSAFYSLPLAPLS--PT 51
                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVPEEQAVRPVSFG-AEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSIPSEALSAVSLQASPGDGSPDFPIVAMLRAPKLWLLPHSTLVPNVSPIPLSPASPLPS 669
                                                                  PR00053; FORKHEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  OF 4-114 FROM N.A.
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944
967
1164
1257
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(Rel. 35,
(Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                 of the mouse forkhead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
 ; FORK_HEAD_1; 1.
; FORK_HEAD_2; 1.
; FORK_HEAD_3; 1.
FORK_HEAD_2;
FORK_HEAD_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35, Created)
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944
967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Last sequence update)
, Last annotation update)
B2 (Transcription factor FKH-4).
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35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
O-LINKED (XYL. . .) (CHONDROITIN SUI
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 81.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                     90:7628-7631(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; E
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                               gene family are developmentally
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RPB1_ARATH
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Best Local
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P18616; P31635; Q95288;
01-NOV-1990 (Rel. 16, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6).
RPB205 OR RPII OR RPB1 OR AT4G35800 OR F4B14.70.
Arabidopsis thaliana (Mouse-ear cress).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaccae; Arabidopsis.
                                                                                                                                                                                                                                                                      MEDLINE=91080867; PubMed=2259344;
Nawrath C., Schell J., Koncz C.;
"Homologous domains of the largest subunit of eucaryotic polymerase II are conserved in plants.";
mol. Gen. Genet. 223:65-75(1990).
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DOMAIN
                                                                                                                                                                                                   Dietrich M.A., Prenger J.P., Guilfoyle T.J.;
"Analysis of the genes encoding the largest subunit of RNA polymerase
"I in Arabidopsis and soybean.";
                                                                                                                                                               STRAIN=CV.
                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                            Plant Mol.
                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
MEDLINE=91355869; PubMed=2103447;
                                                                                                                                                                                                                                            STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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DNA_BIND
                                                                                                                                                    MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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15:207-223(1990).
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No. 0.81;
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RA Pettett A. Rajandream M.A. Lyne M., Benes V., Rechmann S., Argandream M.A. Lyne M., Benes V., Rechmann S., Bosecker H., Scharfe M., Gramm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Massenet O., Quidjey F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quidjey F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Frishman D., Haase D., Lemcke K., Mewes H. W., Stocker S.,
RA Frishman D., Haase D., Lemcke K., Mewes H. W., Stocker S.,
RA Frishman D., Haase D., Lemcke K., Mewes H. W., Stocker S.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
The Hallian T., Martienssen R., McCombie W.R.;
The Hallian T., Martienssen R., McCombie W.R.;
The Hallian T., Till S.,
The Hallian T., Martienssen R., McCombie W.R.;
                                                                                                                                                                                                                                                              EMBL; X52954; CAA37130.1; -.
EMBL; X52494; CAA36735.1; -.
EMBL; AL03196; CAA21466.2; -.
EMBL; AL161588; CAB81489.1; -.
PIR; S12071; JDMUI.
PIR; S11960; JDMUZ.
 CONFLICT
                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                Transferase;
                                                                                                                                                               Pfam; PF00623; RNA_pol_A; 1 Pfam; PF01854; RNA_pol_A2;
                                                                                                                                                                                                 InterPro; IPR000684; RNA_polII_repeat
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
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-!- FUNCTION: DNA-DEPENDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and analysis thaliana.";
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MISCELLANGOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
                                                                           BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERA III FOR 5S AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF DNA INTO RNA USING
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                                                                                                                                                 PS00115; RNA_POL_II_REPEAT; 23.
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                                                                                                              DNA-directed RNA polymerase; Transcription; Zi Nuclear protein; Phosphorylation; Zinc-finger.
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                 ALPHA-AMANITIN BINDING.
CARBOXYL-TERMINAL 7-RESIDUE
MISSING (IN REF. 2).
                                                                       C2H2-TYPE (POT
BY SIMILARITY.
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NSKEE (IN REF.
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                                                                                             (POTENTIAL).
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Q9R172;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
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                                                                                                                                                                        development."
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                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                                                                                                                                                    functional roles
                                                                                                                                                                                                 "Expression
                                                                                                                                                                                                                                     TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                               Neuron
                                                                                                                                                                                                                                                                                     "Notch1 and Notch3 instructively restrict bFGF-responsive multipotent
                                                                                                                                                                                                                                                                                                            Tanigaki K.,
                                                                                                                                                                                                                                                                                                                                                                         "Rattus norvegicus
                                                                                                                                                                                                             Irvin D.K.,
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           suppression.
SUBUNIT: Het
terminal fra
                                                                                           FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl, Jaggedl and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus.
                                               Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). Acts instructively to control the cell fate determination of COS multipotent progenitor cells, resulting in astroglial induction and neuron/oligodendrocyte
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                                                                                                                                                                                                                                                            progenitor cells to an astroglial fate."; 29:45-55(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                             Neurol. 436:167-181(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         739
1062
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                                                                                                                                                                                  31789; PubMed=11438922; Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.; Patterns of Notch1, Notch2, and Notch3 suggest multiple roles for the Notch-DSL signaling system during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence up)
(Rel. 41, Last annotation)
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          Heterodimer of a fragment N(EC) wh
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                                                                                                                                                                                                                                                                                                             Takahashi
                                                                                                                                                                                                                                                                                                                                                           Weinmaster G., Schanen N.C. Notch 3.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
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E -> R (IN REF. 2).
KELVDYGPHPPPGKTGA ->
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Sciurognathi; Muridae
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A -> P (IN REF.
Y -> YSPTSPSY (I
                        C-terminal fragment N(TM) and a N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  otation update)
protein 3 precursor (Notch
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-> P (IN REF. 2).
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           probably
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            disulfide
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JR Pfam; PFUUUL;
JR Pfam; PFOU066; notch; 3.

OR Pfam; PFO0066; notch; 3.

DR PRINTS; PRO0011; EGFBLOOD.

DR PRINTS; PRO0011; EGFLAMININ.

DR PRINTS; PRO1452; NOTCH.

DR SMART; SM00179; EGF_CA; 20.

SMART; SM00004; NL; 3.

DR SMART; SM00004; NL; 3.

DR PROSITE; PS0098; ANK_REP_REGION; 1.

PROSITE; PS00010; ASX_HYDROXYL; 18.

PROSITE; PS00010; ASX_HYDROXYL; 18.

PROSITE; PS01018; EGF_1; 26.

DR PROSITE; PS01187; EGF_CA; 17.

PROSIT
              InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR000800; Notch.
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: Phosphorylated (By similarity).
SIMILARITY: BELONGS TO THE NOTCH FAMILY.
SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to ventricular germinal zones.

PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentil dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - burden Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit institute.
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P00740; 1E
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PF00023; ank; 6.
PF00066; notch; 3.
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  NOTCH EXTRACELLULAR TUNCATION IN THE SIMILARITY).

NOTCH INTRACELLULAR DOMAIN (ISIMILARITY).

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 4, CALCIUM-BINDING
                                                                                                                                                                                                                      POTENTIAL.

POTENTIAL.

NEUROGENIC LOCUS NOTCH HOMOLOG

NEUROGENIC LOCUS NOTCH HOMOLOG

NOTCH EXTRACELLULAR TRUNCATION
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       CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                        (BY
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01-OCT-1994 (Rel. 30, L
15-DEC-1998 (Rel. 37, L
Hypothetical 92.8 kDa p
YBR108W OR YBR0901.
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                                                                                                                                                                                                                                                                                      Hypothetical
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SGD; S0000312; YBR108W.
                                                                                                                                                                                                                                                                                                                                                    EMBL; X78993; CAA55611.1; -. EMBL; Z35977; CAA85063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.; "Analysis of a 70 kb region on the right arm of yeast chro Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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443
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                                         63 GPDPDAH 69
                                                                                                                              13 PVPLRMQPGPAHPV----LSFLRPSWDLVSA---FYSLPLAPLSPTSVP---ISPVSVGR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
LPPPPTH
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2; Mismatches
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5; Mismatches
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PHO88-CMD1 intergenic region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                            10;
                                                                                                                                                                        Gaps
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RESULT

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PER2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                    FACTOR. BEHAVES AS A MEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTION
FACTOR. BEHAVES AS A MEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL
LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT
TRANSCRIPTIONAL INHIBITION. EXPRESSION OSCILLATES WITH A 24 HR
RHYTHM IN THE SUPRACHIASMATIC NUCLEUS (SCN) AND THE WHOLE EYES.
OSCILLATIONS ARE MAINTAINED UNDER CONSTANT DARKNESS AND ARE
RESPONSIVE TO CHANGES OF THE LIGHT/DARK CYCLES. THERE IS A 4 HOUR
TIME DELAY BETWEEN PERI AND PER2 OSCILLATIONS. THE EXPRESSION
RHYTHMS APPEAR TO ORIGINATE FROM RETINA (BY SIMILARITY).
-!- SUBCELULUAR LOCATION: NUCLEAR (POTENTIAL).
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED. FOUND IN HEART, BRAIN,
PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS.
-!- INDUCTION: BY LIGHT (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97349984; PubMed=9205841;
Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII.

"Prediction of the coding sequences of unidentified human genes. VII.

The complete sequences of 100 new cDNA clones from brain which can
                                                                                  SMART;
 Transcription regulation;
DOMAIN 109 146
DOMAIN 182 248
                                                                                                                                                                       EMBL; AB002345; BAA20804.2;
                                                                                                                                                                                                        or send an
                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the suprachiasmatic nucle
Neuron 19:1261-1269(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., I
Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Las
15-JUN-2002 (Rel. 41, Las
Period circadian protein
PER2 OR KIAAO347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      015055;
15-JUL-1999
                                                  PROSITE; PS50112; PAS;
                                                                    SMART;
                                                                                                     InterPro; IPR001610; PAC
InterPro; IPR000014; PAS
                                                                                                                                      MIM; 603426;
                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reppert S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shearman L.P., Zylka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98087121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PER2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Two period homologs: circadian expression and photic regulation
                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e for large proteins in vitro."; Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                    SM00091; PAS;
                                                                                     SM00086; PAC;
                                                                                                                                                    HGNC:8846;
                                                                                                                                                                                                                                                         non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishikawa K.-I.,
., Kotani H., No
                                                                                                                                                                                                     equires a license agreement (See email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                      PER2.
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lka M.J., Weaver D.R.,
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                                                                                                                                                                                                                                                         institutions as long
                                                                                                     PAS_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nomura N.,
Nuclear protein; Repeat; Biological rhythms. HELIX-LOOP-HELIX MOTIF (BY SIMILARITY). PAS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seki N., Nakajima D.,
                                                                                                                                                                     ALT_INIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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YC18_HUMAN
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Best Local
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or send a
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DOMAIN
                                                                                                                                    SEQUENCE
                                                                                                                                                                               Hypothetical NON_TER
                                                                                                                                                                                                    EMBL; AB033044; BAA86532.1; -.
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20039619; Pu
Nagase T., Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           Ohara O.
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                 "Prediction of the coding sequences of unidentified human genes. XV The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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563
                                            517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         863 GTVAAPPAPPHASFTVPAVPVDLQHQFAVQPPPFPAPLAPVMAFMLPSYSFPSGTPNLPQ
                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
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                                                                                                                                                                                                                                                         European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE ATAXIN 7 FAMILY.
                                                                                                                                                                                                                                                                                                                             large proteins in vitro. Res. 6:337-345(1999).
SAMLSNAAFVTSPDPSALMSHTTAFPHVAATLS 595
                                                              SLLPRPAA----VPVPLR-MQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSP-----
                   SVPISPVSVGRGPDPDA------HVAVNLS
                                           SPLPSPAAHITTPVPASVLQP
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                                                                                                                                                                                                                        s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                  Similarity
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                                                                                                                                                                                                                                               non-profit institutions as long and this statement is not removed.
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                                                                                                                                              223
652
786
                                                                                        Conservative
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                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Last sequence update) (Rel. 40, Last annotation update) protein KIAA1218 (Fragment).
                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10574462;
wa K.-I., Kikuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40,
                                                                                                                                  226 P
664 P
790 P
92138 MW;
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438
513
806
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25.6%;
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35.5%;
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                                                                                                                                 POLY-THR.
POLY-SER.
POLY-SER.
DE5CE8130E48DA23 CRC64;
                                                                                                 Score 73.5;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74.5;
Pred. No. 8.
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                                                                                      Mismatches
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                                            FSNP----
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                     75
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                                                                                                             DВ
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                                          SAVY-LPSAPISSRLTSSYIMT 562
                                                                                     21;
                                                                                                          1;
                                                                                                                                                                                                                                              Usage
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                                                                                                                                                                                                                                                                               and the
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                                                                                      35;
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                                                                                    Gaps
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RESULT 9
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Best Local
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CARBOHYD
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070141;
                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 16-OCT-2001 (Rel. 40,
                                                                                                                       SEQUENCE
                                                                                                                                              CARBOHYD
                                                                                                                                                          CARBOHYD
                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                      Signal;
                                                                                                                                                                                                                                                                                                                 Pfam; PF01403; Sema; SMART; SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB000776; BAA25687.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         semaphorin Z.";
Brain Res. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEMA6B.
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                                                                                                                                                                                                                                                                                          Developmental protein
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003659;
InterPro; IPR001627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98087397; PubMed=9427525;
Kikuchi K., Ishida H., Kimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Wistar; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Semaphorin 6B
                          699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular cloning of a novel member of semaphorin family genes,
  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein.

DEVELOPMENTAL STAGE: DETECTED IN THE FIRST BACHIAL ARCH OF EMBRYON DAY 11 (E11) EMBRYO. AND SUBSEQUENTLY IN THE MYOTOMES AND THE DORSAL ROOT GANGLIA IN DEVELOPING SOMITES FROM E11.5

THROUGH E13.5, BUT NOT IN THE BRAIN. HOWEVER, AT E15, 18, 21 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PO, SEMAZ WAS HIGHLY EXPRESSED IN THE BRAIN. SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY. SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION:
SVPIS-PVSVGRGPD
                         GPHDLDSGLLPTPEQTPLPQKRLP-TTHPHAHALGPRAWDHSHALLSASASTSLLLLAHT 757
                                               GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT 51
                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                     Similarity
                                                                                                                       887
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. Brain Res. 51:229-237(1997).
MAY PLAY A ROLE IN BOTH PERIPHERAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor
                                                                                                                       ΑA;
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887
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                                                                                  17.6%;
 65
                                                                                                                                                                                                                                                                                                                                          Sema.
                                                                                                                                                                                                                                                                                                                                                      Plexin-like.
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Last annotation update)
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09543F3F202CD301
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Pred. No. 7.5;
6; Mismatches
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NK4R_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Leves Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A., Sanseau P., Pollinsky R.J., Wasco W., da Silva H.A.R., Hain Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P49750; P49752; Q9P1V7;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation
Nuclear protein ZAP3 (ZAP113).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease.";
Nature 375:754-760(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95319502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frameshift in position 1661.
                                                                PRPALLPTPVSFGSAPPTTYHPPLQSAGPSEQVNSK-----APLSKSALPYSSFSSDQG 524
                                                                                                  PRPAAVPVPLRMQPGPA---HPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRG
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L40400;
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                                                                                                                                      Mismatches
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MEDLINE=97103087; PubMed=8947459;
Donaldson L.F., Haskell C.A., Hanley M.R.;
"Functional characterization by heterologous expression cloned tachykinin peptide receptor.";
Biochem. J. 320:1-5(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neuromedin K receptor (NKR) (Neurokinin B receptor) (NK-4 receptor)
(NK-4R) (K1R) (Neurokinin 4 receptor) (NK4).
TACR3L OR TAC3RL OR TC4R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
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  DISULFIL
                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00237; PROSITE; PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M84605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Expression cloning of cDNA encoding a seven-heli human placenta with affinity for opioid ligands." Proc. Natl. Acad. Sci. U.S.A. 89:4124-4128(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
MEDLINE=92237319;
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P30098;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn.
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TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE, LIVER,
LUNG AND HEART. LOW LEVELS IN PANCREAS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST TO OTHER TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAUTION: Was originally (Ref.1) thought to
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G_PROTEIN_RECEP_F1_2; 1.
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EXTRACELLULAR (
7 (POTENTIAL).
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3 (POTENTIAL).
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Best Local :
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SOX6_HUMAN STANDARD;
P35712; Q9BXQ5; Q9BXQ4; Q9BXQ3; Q9H018;
O1-UUN-1994 (Rel. 29, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription factor SOX-6.
 EMBL;
                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                          "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                          Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glass
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 632-685 FROM N.A. MEDLINE=92310993; PubMed=1614
                                                                                                                                                                                                                                                                                                                                                                                                   Mewes H.-W., Otto
Wambutt R., Korn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lymphocytes, and Myob
MEDLINE=21153434; PubMed=112:
Cohen-Barak O., Hagiwara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Mammalia; 1
                                                                                                                        between
                                                                                                                                                                                                                                                              Nucleic Acids Res. 20:2887-2887(1992)
                                                                                                                                                                                                                                                                              SRY."
                                                                                                                                                                                                                                                                                        Denny P., Swift S., Brand N., Dabhade N. "A conserved family of genes related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21154917; PubMed=11230166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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                                                                                                                                                                                      FUNCTION: BINDS SPECIFICALLY TO THE DNA SEQUENCE 5'-AACAAT-3'.
SUBSCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2, and 3; are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in a wide variety of tissues, most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 THSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSL 43
                                                                                                                                                               abundantly in skeletal muscle. SIMILARITY: CONTAINS 1 HMG BOX.
                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TASPSPAPSWTPSP---RPGPAHP---FLQPPWAV--ALWSL 65
                         AF309034; AAK26115.1; -.
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19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hetazoa;
Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
24
349
440
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nilarity 45.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Ottenwaelder B., Obermaier B.,
AAK26243.1;
AAK26243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
24
349
49431 <sub>1</sub>
                                                                                                                                                                                                                                                                                                                                                                                                    в.,
                                                                                                                                                                                                                                                                                                                    PubMed=1614875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Myoblasts;
ubMed=11255018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                   Klein M., Poustka A.;
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Pred. No. 5;
S; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arlt M.F., Hond chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
PALMITATE (BY SIMILARITY).
544EBJA71CC6C143 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLICING,
                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                     Barton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapping
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                                                                                                                                                                                                                                                                                        arton P.
                                                                                                                                                                                                                                                                                                                                                                                                                Tampe
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ing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 440
                                                                                                                                                                                                                                                                                                                                                                                                                J., Heubner D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                       determining
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                                                                                                                                                                                                                                                                                                     Ashworth A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glassl
                                                                                                                        a collaboration -
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RESULT 13
CBP_MOUSE
ID CBP_M
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Best Local
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                                                                                                                                                                                CBP_MOUSE STANDARI P45481; 01-NOV-1995 (Rel. 32, 0) 01-FEB-1996 (Rel. 33, 15-JUN-2002 (Rel. 41, CREB-bidding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S21481; S21481.
PIR; S22940; S22940.
PIR; S21486; S21486.
HSSP; Q05066; 1HRY.
Genew; HGNC:16421; SOX6.
InterFro; IPRO00910; HMG, PF05055; HMG, Box; SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
                       "Phosphorylated CREB binds specifically Luc L.... "Phosphorylated CREB binds specifically Luc L... "Reduced 365:855-859(1993).

-i- FUNCTION: MEDIATES CAMP-GENE REGULATION BY BINDING FUNCTION: ACCITION AS A COACTIVATE TRA
                                                                       Chrivia J.C.,
Goodman R.H.;
                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                            CREBBP OR CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                              MEDLINE=94019866; PubMed=8413673; Chrivia J.C., Kwok R.P.S., Lamb N.,
                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Nuclear protein; Alternative splicing.
                                                                                                      TISSUE=Brain;
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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CAMP-RESPONSIVE GENES SUBCELLULAR LOCATION:
                   PHOSPHORYLATED CREB PROTEIN. ACTING THE ACTIVITY OF PHOSPHORYLATED CREB
                                                                                                                                                                                                                                                                                                            AHVAVN
                                                                                                                                                                                                                                                                                                                                 AAQPLNLSSRPKTAEPVKSPTSPTQNLFPASKTSPVNLPNKSSIP-SPIGGSLGRGSSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; AF309472; AAK26243.1
; AF309473; AAK26243.1
; AF309474; AAK26243.1
; AF309475; AAK26243.1
; AF309476; AAK26244.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF309474; AAK26244.1;
AF309475; AAK26244.1;
AL136780; CAB66714.1;
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AF309472; AAK26244.
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621
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313
514
327
579
477
633
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184 262
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                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                           32, Created)
33, Last sequence 41, Last anno
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518
518
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                                                                                                                                            Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                   17.1%;
34.8%;
                                                           binds specifically to the nuclear protein CBP.";
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                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  MW.
Nuclear
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ALT_INIT.
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JOINED.
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POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                             Score 71.5;
                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 3).
S -> SLGKWKSQHQEETYE (IN
K -> R (IN REF. 3).
                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMG BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                  58CA7C0DEA811D5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    NO.
                                                                               Hagiwara M.,
                                                                                                                                                                                                                                       2441
                   AS A COACTIVATOR, CBP AUGMEN
TO ACTIVATE TRANSCRIPTION OF
                                                                                                                                                                                                                                       AΑ
                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                               Montminy M
                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                       SPECIFICALLY
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                              ICALLY TO AUGMENTS
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YD53_SYNY3
ID YD53_S
AC P42350
DT 01-NOV
DT 15-JU;
DE Hypott
GN SLR13;
OS Synce;
OX NCBL_'
RN [1]
RP SEQUE
RX MEDLI
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                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Best Local S
Matches 23
                                                                                                                                                                                                 01-NOV-1995 (
01-NOV-1995 (
15-JUN-2002 (
Hypothetical
SLR1353.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=93222488; PubMed=8467083;
Malakhov M.P., Wada H., Los D.A., Sakamoto T.,
"Structure of a cyanobacterial gene encoding t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00297; BROMO; 1.
SMART; SM00291; ZnF_ZZ; 1.
PROSITE; PS00633; BROMODOMAIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000197; TAZ_finge
InterPro; IPR000433; Znf_ZZ.
Pfam; PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S66385; AAB28651.1; -. TRANSFAC; T01318; -. MGD; MGI:1098280; Crebbp.
                                                                                                                                Bacteria; Cyanobacteria;
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                               Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Nuclear protein; Activator; Bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00503; BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001487; Bromodomain.
InterPro; IPR003101; KIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    843
                                                                                                                                                                                                                                                                                                                                                                                                                                              900 PTP 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 BROWODDMAIN.
SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQLPCPPVTQSPLHPTPPPASTAAGM--PSLQHPTAPGMTPPQPAAPTQ-PSTPVSSGQT 899
                                                                                                                                                                                                                                                                                                                                       SYNY3
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PF02135; zf-TAZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50135; ZF_ZZ_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50014; BROMODOMAIN_2; 1.
PS01357; ZF_ZZ_1; 1.
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1702
1062
1556
1944
1968
2082
2200
2296
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(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                         (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                               (strain
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36.5%;
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Znf_ZZ.
                                                                                                                                                           Chroococcales;
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POLY-GLN.
POLY-GLN.
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BROMODOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLN
                                                                                                                                                                               6803)
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0ABB028C3112F419 CRC64;
                                                                                                                                                                                                                                                                                                                                    291 AA
                                                                                                                                                         Synechocystis
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Best Local
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DPOL HPBHE STANDARD;
P13846;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA directed DNA polymerase (EC 2.7.7.7); RNA-
P protein PNA polymerase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)
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J. Virol.
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EMBL; D90912; BAA18174.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 291 AA; 31283 MW; 5AB7E3DD03C36390 CRC64;
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                                                                                                                                            between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
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MEDLINE=88333160; PubMed=3418788,
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                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and characterization of a hepatitis B virus endemic
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                                                                                                                                                                                                                                                                phosphomonoester.
                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; M22056; AAA45738.1; -.

DR PIR; A30082; JDVLHH.

DR InterPro; IPR001462; DNApol_viral_C.

DR InterPro; IPR00201; DNApol_viral_N.

DR Pfam; PF00024; DNA_pol_viral_N; 1.

DR Pfam; PF00028; DNA_pol_viral_C; 1.

DR Pfam; PF00036; DNA_pol_viral_C; 1.

DR Pfam; PF00036; DNA_pol_viral_C; 1.

DR Pfam; PF00336; DNA_pol_viral_C; 1.

DR ProDom; PD000814; DNApol_viral_C; 1.

DR ProDom; PD000814; DNApol_viral_C; 1.

SR ProDom; PD000814; DNApol_viral_C; 1.

DR Prodom; PD000814; DNApol_viral_C; 1.

DR Prodom; PD000814; DNApol_viral_C; 1.

CW Transferase; RNA-directed DNA polymerase; Nuclease; Endonuclease; DNA replication; DNA-binding.

KW Transferase; RNA-directed No. 13; DNA replication; DNA-binding.

SQ SEQUENCE 788 AA; 90070 MW; FB44F38F75EADF44 CRC64;

Query Match

Best Local Similarity 40.0%; Pred. No. 13;

Matches 18; Conservative 4; Mismatches 12; Indels 11; Gaps 1;

Matches 18; Conservative 4; Mismatches 12; Indels 11; Gaps 1;

DNA PD1 PD POVSURGE P
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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SPTREMBL_21:*

Sp_archea:*

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Sp_bunder:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	341 GTHSLPPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 400	Db
	1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60	Qy
0	Query Match 97.1%; Score 406; DB 4; Length 419; Best Local Similarity 97.5%; Pred. No. 2.2e-35; Matches 77; Conservative 1; Mismatches 1; Indels 0; Gaps	
	SEQUENCE 419 AA; 45472 MW; FEC1BE347E2D030C CRC64;	SQ
	PF01030; Recep_L_dom	DR:
	InterPro; IPR002174; Furin-like. Pfam: PF00757: Furin-like: 1	DR DR
	InterPro; IPR000494; EGFR_L_domain.	DR
	SUBMITECE (SEF-2000) TO THE EMBL/GENBANK/DDBJ GATADASES. FMBI- ART17161. ANDS6AO0 2.	2 2
		P RA
	SEQUENCE FROM N.A.	RP
		RN
	Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999).	RL
		RŢ
	"The HER-2/neu receptor tyrosine kinase gene encodes a secreted	RT :
	Doherty I K Bond C Jardim A Adelman I D Clinton G M	RA
		굔 :
		R S
	NCB1_TAX1U=9606;	N C
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	Eukaryota; Metazoa; Chordata;	8
	Homo sapiens (Human).	SO
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GRGPDPDAHVAVDLSRYEG GRGPDPDAHVAVNLSRYEG

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                                                                        ID ACCOMENDATION ACCOMENDATION OF THE REAL REPORT O
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Best Local S
Matches 30
Query Match
Best Local
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01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Hypothetical 31.5 kba protein.
Grapevine fleck virus.
Viruses; unclassified viruses.
                                                                                                                                                                                                                                                                                                                                                                                         Q99JK6 PRELIMINARY; PRT; 327 AA.
Q99JK6;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 33.7 kDa protein (Fragment).
                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006054; AAH06054.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8UZB4
                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sabanadzovic S., Abou Martelli G.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MT48;
                                                                                              NON_TER
                                                                                                                 Hypothetical protein.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fleck virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21351056; PubMed=11458008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sabanadzovic S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=103722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete nucleotide sequence and
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  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPRPAAVPV-----PLRMQPGP-AHPVLS-----FLRPSWDLVSAFYSLPLAPLSPTS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPISPVSVGRGPDPDAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPRSVAFPLPLARELPPLRLPPAPYLHPLLARLAPLRLRPPPDLPSP----PLSP--PLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ309022; CAC84402.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virol. 82:2009-2015(2001).
J309022; CAC84402.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                      AA;
                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                      33661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.8%;
  20.3%;
42.4%;
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20, Last sequence update)
20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
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8; Mismatches
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  Score
Pred.
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Sciurognathi;
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                                                                   27917F16D583E774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E40F68A7F54737B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome organisation of Grapevine
  NO .
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  DB 11;
0.28;
                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
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                        Length 327;
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                                                                                                                                                                                                                                                                                                                                 Murinae;
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Best Local S
Matches 26
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Q9GU15; CTEMBLrel. 16, Crea
01-MAR-2001 (TrEMBLrel. 16, Last
01-DEC-2001 (TrEMBLrel. 19, Last
01-DEC-2001 (TrEMBLrel. 19, Last
Profile Company 
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O35615;
O1-JAN-1998
O1-JAN-1998
O1-MAR-2002
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20520968; PubMed=11071289;
Bishop R., Gobright E., Nene V., Morzaria S., Musoke A., Sohar
Bishop R., Gobright E., Nene V., Morzaria S., Musoke A., Sohar
-- ''...ornhic open reading frames encoding secretory proteins of the secre
differentiation.";
Cell 90:109-119(1997).
-!- SUBCELLULAR LOCATION:
EMBL; AF006492; AAC53292.
                                                                                                                                                                                                       Tsang A.P., Visvader J.E., Turner C.A. Weiss M.J., Crossley M., Orkin S.H.; "FOG, a multitype zinc finger protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biochem. Parasitol. 110:359-37: EMBL; AF225701; AAG28022.1; -. InterPro; IPR002965; P_rich_extensn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                          transcription factor GATA-1 in
                                                                                                                                                                                                                                                                                                                                       MEDLINE=97373824; PubMed=9230307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZFPM1 OR FOG.
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Metazoa; Rodentia; C
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3 (TrEMBLrel.
2 (TrEMBLrel.
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Pred.
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No. 0.43;
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Best Local :
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R InterPro; IPR001005; Myb_DNa_binding.

R InterPro; IPR000822; Znf_C2H2.

R Pfam; pF00096; Zf-C2H2; 9.

R PRINTS; PR00048; ZINCFINEER.

R PRINTS; SM00355; Znf_C2H2; 5.

R PROSITE; PS00037; MYB_1; UNKNOWN_1.

R PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_2.

R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.

R PROSITE; PS00157; ZINC_FINGER_C2H2_2; 2.

NDNA-binding; Nuclear protein; Zinc-finger.

DNA-binding; Nuclear protein; Zinc-finger.
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Best Local 9
                                                                     O91115
Q91115;
Q91115;
01-DEC-2001 (TrembLrel. 1
01-DEC-2001 (TrembLrel. 1
01-MAR-2002 (TrembLrel. 2
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01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
0034C09.31 protein.
00034C09.31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-39947;
                                   ORF3 protein.
Hepatitis E virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone:P0034C09.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AP003450; BAB84618.1;
Viruses; ssRNA positive-strand viruses, Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Oryza sativa nipponbare(GA3)
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                                                                                                                                                                                                                                                   PGSTRH
                                                                                                                                                                                                                                                                                         PDPDAH
                                                                                                                                                                                                                                                                                                                         TLLSSPTPVVVPM-LLPSPTRPVVFSMQPHFDLVPA----LPPSSP-QVPQSSLSSLSA 106
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                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Last annotation update)
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Pred. No. 1.2;
10; Mismatches
                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                  Score 82.5; D
Pred. No. 0.51
8; Mismatches
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Best Local
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Best Local 9
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Virology 287:9-12(2001).
EMBL; AP003430; BAB63940.1; -
InterPro: IPR003384; HEV_ORF2;
Pfam; PF02444; HEV_ORF2; 1.
SEQUENCE 122 AA; 12313 MW; [
                                                                                                                                                                                                EMBL; InterPro; ir...
InterPro; ir...
Fram; PF02444; HI
Tram; PF02444; HI
Tram; PF02444; HI
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Q8V730;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                      isolated in Japan.";
Biochem. Biophys. Res. Commun.
EMBL; AB073912; BAB79305.1; -.
Interpro; IPR003384; HEV_ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphoprotein.
Swine hepatitis E virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses,
NCBI_TaxID=63421;
                                                                                                                                                                                                                                                                                                                                                           Okamoto H., Takahashi M., Nishizawa
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SWJ570;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21396683; PubMed=11504536; Takahashi K., Iwata K., Watanabe N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12461; [1]
                                                                                                                                                                                                                                                                                                                                           Yoshikawa A.;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21616952; PubMed=11741279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=JRA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JRA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     "Analysis of the complete genome of indigenous swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Full-genome nucleotide sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 V
                 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPL---SPTSVPISP
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                                                     GVTGLILSPS--PSPIFIQPTPS-PPMSFHNPGLELALDSRPAPLAPLGATSPSAPPLPP 111
                                                                                     GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPL---SPTSVPISP
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                 58
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                                                                                                                                                Similarity
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                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                      HEV_ORF2; 1.
AA; 12397 MW;
                                                                                                                                                19.6%;
37.7%;
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37.7%;
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                                                                                                                            Score 82; DB Pred. No. 0.21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence up
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                               289:929-936(2001)
                                                                                                                                                                                                        6BAA9F02321D26A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D6C56A8E54C587DD CRC64;
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                                                                                                                                              DB 12; Length 122;
).21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA stage
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                                                                                                                              22;
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Pfam; PF000059; lectin_c; 1.
Pfam; PF00193; xlink; 1.
PRINTS; PR001019; EGFBLOOD.
PRINTS; PR01265; LINKMODULE.
PRODOM; PD000918; Link; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM000445; LINK; 1.
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070474;
01-AUG-1998 (TrEMBLTel. C
01-AUG-1998 (TrEMBLTel. C
01-JUN-2002 (TrEMBLTel. 2
                                               01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_3.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01141; LINK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
HSSP;
            AT2G31050.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                     082761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY: TISSUE-HIPPOCAMPUS Zachmann-Brand B., Schaller H.C.;
                                  Putative phytocyanin
                                                                                                    082761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurocan (Fragment).
 Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                 Calcium-binding; EGF-like domain; Glycoprotein; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001304;
InterPro; IPR000538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                402
                                                                                                                                                                                                              342
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                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                     4 SLLPRPAAVPVPLRMQPG---PAHPVLSFLR-----PSWDLVSAFYSLPLAPLS--PT 51
                                                                                                                                                                                    SVP----ISPVSVGRGPDPD
                                                                                                                                                             SVPEEQAVRPVSFG-AEDPE 420
                                                                                                                                                                                                              SSIPSEALSAVSLQASPGDGSPDFPIVAMLRAPKLWLLPHSTLVPNVSPIPLSPASPLPS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P00740;
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                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                              816 AA;
                                                                                                  PRELIMINARY;
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                                 el. 21, Last annotation update) (Putative blue copper-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Link.
                                          08, Created)
08, Last sequence update)
21, Last annotation updat
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07,
21,
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                           Pred. No. 1.7;
0; Mismatches
                                                                                                                                                                                                                                                                        Score 81.5;
Pred. No. 1
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                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                            957F5917AD10616E CRC64;
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Embryophyta; Tracheophyta;
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Q9LMQ1;
Q9LMQ1;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-JUN-2002 (TrEMBLrel. 21, L
F7H2.17 protein.
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Best Local
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Town C.D., Kaul S.;
Submitted (FEB-2002) to the EN
EMBL; AC005311; AAC63847.1; --
EMBL; AC004669; AAM14981.1; --
HSSP; P00303; 2CBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
  SEQUENCE FROM N.A STRAIN=CV. COLUMB: Liu S.X., Sakano I
                                                                                             Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Bras NCBI_TaxID=3702;
                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003245; Plcyanin_like. Pfam; PF02298; Cu_bind_like; 1. ProDom; PD003122; Plcyanin_like; 1. SEQUENCE 200 AA; 21475 MW; E669
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ROUNSley S.D., Kaul S., Lin X.,
Brandon R.C., Sykes S.M., Mason
Somerville C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 PAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDPDA
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                         COLUMBIA;
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     Η.,
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34.3%;
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Last annotation updat
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Pred.
                                                                                                                                                                                                                                                                                                                                                                             PRT;
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T.M., Kerlavage A.R., Adams M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                            Arabidopsis
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Best Local
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01-OCT-2000
01-MAR-2002
Rao P., Jiang H., Wang F.; "Cloning of the rhesus lymphocryptovirus viral capsid antigen and Epstein-Barr virus-encoded small RNA homologues and use in diagnos of acute and persistent infections."; J. Clin. Microbiol. 38:3219-3225(2000).
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                                                                                                                                                                                      STRAIN=LCL8664;
MEDLINE=20304984; PubMed=10846073;
                                                                                                                                                                                                                                                                                                                                                "Comparative analysis identifies conserved tumor n receptor-associated factor 3 binding sites in the Epstein-Barr virus oncogene LMP1.";
J. Virol. 70:7819-7826(1996).
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                 MEDLINE=20440633; PubMed=10970361;
                                                                                  SEQUENCE FROM N.A. STRAIN=LCL8664;
                                                                                                                                                                                                                                   Rivailler P., Quink C., Wang F.;
"Strong selective pressure for evolution of an Epstein-Barr virus LMP2B homologue in the rhesus lymphocryptovirus.";
J. Virol. 73:8867-8872(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaherpesvirinae;
NCBI_TaxID=104228;
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                                                                                                                       Lymphocryptovirus.";
J. Virol. 74:5921-5932(2000).
                                                                                                                                              nuclear antigen 3A,
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Q1-DEC-2001
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01-MAY-1999 (TrEMBLrel. 10, La
01-DEC-2001 (TrEMBLrel. 19, La
Hypothetical 12.4 kDa protein.
Hepatitis E virus.
STRAINS=HEV-US2;
MEDLINS=98178637; PubMed=9519822;
Schlauder G.G., Dawson G.J., Erker J.C.,
Smalley D.L., Rosenblatt J.E., Desai S.M.
"The sequence and phylogenetic analysis o
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Submitted
                                                                                     Viruses; ssRNA positive-strand Hepatitis E-like viruses.
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"Complete Nuclectide Sequence of the Rhesus Lymphocryptovirus: Genetic Validation for an Epstein-Barr Virus Animal Model.";
J. Virol. 76:421-426(2002).
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SEQUENCE FROM N.A.
STRAIN=LCL8664;
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tted (JUN-2001) to the EMBL/GenBank/DDBJ
AY037858; AAF78881.2; -.
NCE 941 AA; 103089 MW; EA4E3DC9BEC19/
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EMBL: AF071081; AAD41594.1; -.
InterPro; IPR002951; Atrophin.
InterPro; IPR003882; Plistil_extensin.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01222; ATROPHIN.
PRINTS; PR01221; KV33CHANNEL.
PRINTS; PR01217; PRCHEXTENSIN.
PRINTS; PR01218; PSTLEXTENSIN.
SEQUENCE 763 AA; 75035 MW; 39168EC4
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Erker J.C., Desai S.M., Schlauder G.G., Dawson G.J., Mushahwar I.K.;
"A hepatitis E virus variant from the United States: molecular
characterization and transmission in cynomolgus macagues.";
J. Gen. Virol. 80:681-690(1999).
                                                                                                                                                                                                                                                                                       Espitia C., Laclette J.P., Mondragon-Palomino M., Amador A., Campuzano J., Martens A., Singh M., Cleero R., Zhang Y., Moreno C. "The PE-PGRS glycine-rich proteins of Mycobacterium tuberculosis: new family of fibronectin-binding proteins?";
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NCBI_TaxID=1773;
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Last annotation update)
                                                                                                    Pred. No. 3.8, 4; Mismatches
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                             Conservative
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Last annotation updat
                                                                                                                                                                                                                                                                                                                 Score 77.5;
Pred. No. 2
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Search completed: March 4, 2003, 12:35:58 Job time: 10.7249 secs

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59, Appl 62, Appl 62, Appl 63, Appl 64, Appl 3, Appl 3, Appl 3, Appl 21, Appl 21, Appl 21, Appl 21, Appl 31, Ap

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 0.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_CTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                    US-09-630-155-1
US-09-630-155-2
US-08-340-428B-49
US-08-462-606-65
US-08-468-576B-12
US-08-468-577B-12
US-08-468-577B-12
US-08-961-739-2
US-08-961-739-2
US-08-961-739-2
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US-09-161-736-11
US-08-615-170-21
US-09-461-697-58
US-09-461-697-58
US-09-461-697-58
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2 1, Appli 2 4, Appli 3 6, Appli 3 9, Appli 3 12, Appli 2 12, Appli 3 12, Appli 3 14, Appli 3 15, Appli 3 15, Appli 3 16, Appl
                                                                                                                                                                                   TOPOLOGY: unknown

HER-2 ECD antagonist
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-630-155-1
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                                                                                                                Query Match
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Matches 79
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                                                                                                                                                                                                                                                                                                                                              TELEFAX: 206 628-7699
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: WINDOWS95
SOFTWARE: WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/630,155
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UDKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Davison, Barry L.
REGISTRATION NUMBER: 47,309
REGISTRATION INFORMATION:
TELEPHONE: 206 628-7621
TELEPHONE: 206 628-7621
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CORRESPONDENCE ADDRESS:
DAVIS WRIGHT TREMAINE
ADDRESSEE: DAVIS WRIGHT TREMAINE
ADDRESSEE: DAVIS WRIGHT TREMAINE
ADDRESSEE: DAVIS WRIGHT TREMAINE
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                                                          GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV
  GRGPDPDAHVAVNLSRYEG
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                                    GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
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79; Conser
                                                                                                                                                                                                                                                                   LENGTH: 79
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER: PC compatible
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                                                                                                              100.0%; ilarity 100.0%; Conservative 0
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US-09-462-606-60
US-09-462-606-63
US-09-462-606-64
US-09-462-606-64
US-09-462-776-3
PCT-US93-08849-3
PCT-US93-08849-3
US-08-240-449B-19
US-08-477-292-21
PCT-US95-13703-21
US-08-451-3
US-08-818-111-143
US-08-818-111-143
US-09-072-596-138
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Pred. No. 5.2e-42;
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Result No.

Score

Match Query

Length

ВВ

418 418 81.5

0;

Gaps

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Database

Minimum Total number

DB DB

seq

length:

length: 2000000000

Sequence:

Perfect score: Title:

US-09-234-208B-1

Scoring table:

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RESULT 2
US-09-630-155-2
; Sequence 2, Application US/09630155
; Patent No. 6414130
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                  RESULT 3
                               Patent NO. 304001.

GENERAL INFORMATION:

APPLICANT: MARGOLIS, Richard U.

APPLICANT: RAUCH, Uwe

APPLICANT: MARGOLIS, Renee K.

TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A

TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN

TITLE OF SECOUENCES: 49
                                                                                                                                                                                                             Sequence 49, Application US/08340428B Patent No. 5648465
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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TELEPHONE: 206 628-7621
TELEFAX: 206 628-7699
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                           401 GRGPDPDAHVAVNLSRYEG 419
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                     STREET:
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FILING DATE: 16-Jan-2001
CLASSEFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORD CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Doherty, Joni Kristin and Gail M. Clinton TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: PC compatible OPERATING SYSTEM: Windows95
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Davison, Barry L. REGISTRATION NUMBER: 47,309 REFERENCE/DOCKET NUMBER: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown ULE TYPE: polypep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1501 Fourth Avenue, 2600 Century Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
                     419 Seventh Street, N.W.
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nilarity 100.0%;
Conservative (
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Pred. No. 4.2e-41;
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; MOLECULE TYPE: peptide US-08-340-428B-49
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                                                                             ; ORGANISM: Hepatitis E virus US-09-462-606-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-462-606-65
                                                                                                                                                PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 65, Application US/09462606 Patent No. 6432408
Query Match
Best Local Similarity
Matches 22; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                      CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 60/053069
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: PCT/US98/1466
                                                                                                                                                                                                                                                                                     APPLICANT: MENG, XIANG-JIN
APPLICANT: Emerson, Suzanne U.
APPLICANT: Emerson, Suzanne U.
APPLICANT: PUTCEL1, ROBERT H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
FILE REFERENCE: 20264267US1
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                TYPE: PRT
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REGISTION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MAJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 1257 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                ENGTH: 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610 SSIPSEALSAVSLQASPGDGSPDFPIVAMLRAPKLWLLPHSTLVPNVSPIPLSPASPLPS 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 SVPEEQAVRPVSFG-AEDPE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/922,911 FILING DATE: 03 August 1992
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   Conservative
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                   18.4%; Score 77; DB 4, 36.1%; Pred. No. 0.067;
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   10; Mismatches
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                                         DB 4;
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   23;
                                         Length 122;
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Sequence 12, Application US/08468576B Patent No. 5955345
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC IS
TITLE OF INVENTION: OBTAINED BY M
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
                                                                                                                                                                                                                                                                                                                    ORIGINIEM: HOMO .
ORGANISM: HOMO .
IMMEDIATE SOURCE:
OPB-R
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Uhl, George R.
APPLICANT: Eppler, C. Mark
APPLICANT: Eppler, C. Mark
APPLICANT: Wang, Jai-Bel
TITLE OF INVENTION: Mu-Subtype Opioid Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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TELEFAX: 236687
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                                                                                                                                                                       32 TASPSPAPSWTPSP---RPGPAHP---FLQPPWAV--ALWSL 65
                                                                                                                                                                                                                                           Local Similarity 45.7 hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: RObinson, Joseph R.
REGISTRATION NUMBER: 33,448
CONTROL NUMBER: 0646/1A843-US5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 28-API
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 V 58
                                                                                                                                                                                           2 THSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSL 43
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45.2%;
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 PANCREATIC ISLET CELL ANTIGENS OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/430,286A
                                                                                                                                                                                                                                        ; Score 72; DB 4; Pred. No. 1.3; 5; Mismatches
                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                          Length 440;
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RESULT 7
US-08-468-579B-12
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                                                                                                        Sequence 12, Application US/08468579B
Patent No. 5981700
GENERAL INFORMATION:
APPLICANT: Rabbin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 000
CITY: Tarrytown
CTATE: New York
                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 05-MAY-
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OPERATING SYSTEM: Syste
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                      480 ILSSLN 485
                                                                                                                                                                                                                                                                                                                                                                               421 AAQPLNLSSRPKTAEPVKSPTSPTQNLFPASKTSPVNLPNKSSIP-SPIGGSLGRGSSLD 479
                                                                                                                                                                                                                                                                                                                                                                                                    10 AAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPV--SVGRGPDPD 67
                                 ADDRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                           68 AHVAVN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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Tarrytown
New York
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604 amino acids
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06-JUN-1995
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Pred. No. 2.2;
l3; Mismatches
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Apple Macintosh

System 7.5

Diskette, 3.50 inch, 1.4 Mb storage

10591-5144

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US-08-468-577B-12; Sequence 12, Apr
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Best Local Similarity 34.8
                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 17-FFE-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: O8-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MDI 251.5-KGB TELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07//15,101
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
US 07/441,703
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APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                   480 ILSSLN 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AAQPLNLSSRPKTAEPVKSPTSPTQNLFPASKTSPVNLPNKSSIP-SPIGGSLGRGSSLD 479
COMPUTER: Apple Macintosh OPERATING SYSTEM: System
                                                                                                        CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPV--SVGRGPDPD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 04-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Sys
SOFTWARE: WordPerfect
                                                                                                                                                                                                                                                                                                                                                                                                                                    68 AHVAVN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                     COUNTRY:
                                                                                                                                             STREET:
                                                                                                                                                                ADDRESSEE:
                                                                      10591-5144
                                                                                                                                                                                                                                                                                         2, Application US/08468577B
6001804
                                                                                                                                             E: Sprung Kramer Schaefer & Briscoe 660 White Plains Road
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O6-JUN-1995
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System 7.5
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                                   1.4 Mb storage
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RESULT 9
US-08-194-468-2
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Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08194468
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APPLICANT: Montmi
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                    APPLICANT: Montminy, Marc R. TITLE OF INVENTION: COMPOUND TITLE OF INVENTION: RESPONSI TITLE OF INVENTION: RESPONSI NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MD TELECOMMUNICATION INFORMATION:
                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
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APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 06-JUI
APPLICATION NUMBER: FILING DATE: 10-FEE CLASSIFICATION: 435
                                                                                                                                                                ZIP: 90071
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                                                                                                                         Floppy disk
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                    10-FEB-1994
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                                   US/08/194,468
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ATTORNEY/AGENT INFORMATION:

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TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-194-468-2
                                                                                                    RESULT 11
US-09-514-247A-8
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                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: VARIANT
; LCCATION: (1)...(2441)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-08-961-739-2
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Sequence 8, Application US/09514247A Patent No. 6365361
GENERAL INFORMATION:
APPLICANT: TANABE SEIVAKU CO. LTD. APPLICANT: TANAGUCHI, Tomoyasu APPLICANT: MIZUKAMI, Junko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Montminy, Marc R.
TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
FILE REFERENCE: SALK1650-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.5
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08961739A Patent No. 6063583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/961,739A CURRENT FILING DATE: 1997-10-31 EARLIER APPLICATION NUMBER: US 194,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619)-546-9392
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                         900
                                                                                                                                                                                                                                       843 SQLPCPPVTQSPLHPTPPPASTAAGM--PSLQHPTAPGMTPPQPAAPTQ-PSTPVSSGQT 899
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                                                                                                                                                                                                        64 PDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192 REFERENCE/DOCKET NUMBER: P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 PDP 66
                                                                                                                                                                                                                                                         4 SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRG 63
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                                                                                                                                                                         PTP 902
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36.5%;
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36.5%;
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Pred. No. 13;
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Pred. No. 13;
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RESULT 13
US-08-615-170-21
: Sequence 21, Application US/08615170
: Patent No. 5776776
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US-09-147-236-11
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SEQ ID NO 11
LENGTH: 344
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Matches
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LENGTH: 24
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Best Local Similarity
                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Appl. Patent No. 631625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/147,236A CURRENT FILING DATE: 1999-04-08 EARLIER APPLICATION NUMBER: PCT/JP97/03633 EARLIER FILING DATE: 1997-10-09 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TONOUCHI, Naoto
APPLICANT: TSUCHIDA, Takayasu
APPLICANT: YOSHINAGA, Fumihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TAHARA, Naoki
APPLICANT: HAYASHI, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES,
FILE REFERENCE: 6537-011-0PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/514,247A CURRENT FILING DATE: 2000-02-28 PRIOR APPLICATION NUMBER: PCT/JP98/03734 PRIOR FILING DATE: 1998-08-24 PRIOR APPLICATION NUMBER: JP231084/1997 PRIOR FILING DATE: 1997-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Acetobacter xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: TANIGUCHI=6
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                              158 YAAAPQPVATPVP--PQPAPVAPVVAAVAQPVRQERPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900 PTP 902
                                                                                                           202 PAVSSFMAPRP 212
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                                                                                                                                           56 SPVSVGRGPDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 PDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 23; Conserv
                                                                                                                                                                                                   3 HSLLPRPAAVPVPLRMQPGPAHPVLSFL-----RPSWDLVSAFYSLPLAPLSPTSVPI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRG 63
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                                                                                                                                                                                                                                                     Conservative
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36.5%;
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                                                                                                                                                                                                                                                                  Score 69.5;
Pred. No. 1.
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Pred. No. 13;
                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                       DB
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SENERAL INFORMATION:

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US-08-615-170-19; Sequence 19, A
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Best Local Similarity
Watches 21; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-615-170-21
                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNIA...
ZIP: 94105-14>
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TWOTTER: IBM PC compatible
TWOTTER: PC-DOS/MS-DOS
                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: 21:
             APPLICANT: STEWART, Alexandre F.R. APPLICANT: LARKIN, Sarah B. TITLE OF INVENTION: DTEF-1 ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                       APPLICANT:
                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF NUMBER OF SEQUENCES: 32
 NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                           155 SAAPRFWSGPIP--GQPGPSQDIKPFAQPAYPIQPPMPPSLASYE-PLAPLPPAASAVPV 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Heslin, James M. REGISTRATION NUMBER: 29 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                    ), Application US/08615170 5776776
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: Steuart Street Tower, One Market Plaza
San Francisco
SEQUENCES:
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                                                                                                     AZAKIE, Anthony
MAR, Janet H.
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LARKIN, Sarah B.
                                                                       HALL, Deborah E.
                                                                                        FARRANCE, Tain K.G.
                                                                                                                                             ORDAHL, Charles P.
                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAR, Janet H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZAKIE, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FARRANCE, Tain K.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                  DTEF-1 ISOFORMS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                16.6%; Score 69.5; 35.0%; Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                   SEQ ID NO 58
LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5 Patent No.
                                                                                               CURRENT APPLICATION NUMBER: US/
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING TITLE OF INVENTION: CELL DEATH
                                                                                                                                                                                                                                                                                                 APPLICANT: Barney, Shawn APPLICANT: Thomas, Mary Beth
                                                                                                                                                                                                                                                                                                                                        APPLICANT: COGENT NEUROSCIENCE, Inc APPLICANT: Lo, Donald C.
                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                         APPLICANT: Portbury, Stuart APPLICANT: Puranam, Kasturi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 326-24
INFORMATION FOR SEQ ID NO:
                                                                                                                                                          FILE REFERENCE: 10001-005-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 06-FEB-1s
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         APPLICANT: Katz,
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Heslin, James M.
REGISTON NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 SAAPRFWSGPIP--GQPGPSQDIKPFAQPAYPIQPPMPPSLASYE-PLAPLPPAASAVPV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/191,493 FILING DATE: 04-FEB-1994
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/615,170
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ZIP: 94105-1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVS-----AFYSLPLAPLSP--TSVPI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                    58, Application US/09461697
5. 6277974
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                                                                                                                                                                                                                                                                                                                                      Lo, Donald C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 amino acids
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         Lawrence C
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                                                                                                                                      US/09/461,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69.5; D:
Pred. No. 2.5;
11; Mismatches
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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Published_Applications_AA:*

1: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 13, Appl	Sequence 22, Appl	Sequence 10, Appl	Sequence 35, Appl	Sequence 667, App	Sequence 100, App	Sequence 36209, A	Sequence 29, Appl	Sequence 1235, Ap		Sequence 5, Appli	Sequence 159, App	Sequence 21, Appl	Sequence 16, Appl	Sequence 659, App	Sequence 48, Appl	Sequence 52, Appl	Sequence 54, Appl	Sequence 58, Appl	259	'n	Sequence 2, Appli		Sequence 8, Appli	Sequence 7, Appli	Sequence 237, App

ALIGNMENTS

RESULT 1 US-10-036-041-35

CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/08579
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: 60/11300
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
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PRIOR APPLICATION NUMBER: 60/125774
PRIOR APPLICATION NUMBER: 60/125774
PRIOR APPLICATION NUMBER: 60/125774
PRIOR APPLICATION NUMBER: 60/125774 Sequence 35, Application US/10036041 Publication No. US20020192751A1 GENERAL INFORMATION: APPLICANT: APPLICANT:
APPLICANT: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME APPLICANT: APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan L. APPLICANT: APPLICANT: APPLICANT: FILING DATE: APPLICATION Goddard, Audrey Godowski, Paul Zhang, Zemin Gurney, Austin L. Wood, William I. Stewart, Timothy A. Pan, James Watanabe,Colin K.

APPLICATION NUMBER:

60/125826

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APPLICATION NUMBER: PCT/US99/28551
APTITING DATE: 1999-12-02
APTITING DATE: 1999-12-07
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PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR ETLING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-07-09
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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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                                                                       PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
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TITLE OF INVENTION:
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                                 APPLICATION NUMBER: 60/0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, Victoria
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APPLICANT: Eaton, Dan L.
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin
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PRIOR APPLICATION NUMBER:
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/131270
FILING DATE: 1999-04-27
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FILING DATE: 2000-12-20
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: 2001-02-28
                                                                                         APPLICATION NUMBER: PCT FILING DATE: 2000-08-24
                                                                                                                         FILING DATE:
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NUMBER: 09/869599
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757 RAPEQPPAPGE-PTPDGRL 774

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; SEQ ID NO 544
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-544
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; ORGANISM: Homo Sapien
US-10-035-855-35
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LENGTH: 888
                                                                                                                                                        Query Match
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Best Local Similarity
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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR EILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C17
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PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
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                                                698 GPHDLDSGLLPTPEQTPLPQKRLPTP-HPHPHALGPRAWDHGHPLLPASASSSLLLLAPA 756
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52 SVPISPVSVGRGPDPDAHV 70
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                                                                                  1 GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT 51
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                                                                                                                                        Similarity
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Wood,William
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o. US20030022239A1
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Pred. No. 0.91;
7; Mismatches 33;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 544
LENGTH: 888
TYPE: PRT
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Best Local :
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nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT 51
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                                                                              Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                          Smith, Victoria Stewart, Timothy A.
                                                                                                                                               Gerritsen, Mary E.
                                                                                                                                                                                Desnoyers, Luc
Filvaroff, Ellen
Watanabe,Colin K
Wood,William
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                                Tumas,Daniel
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Godowski, Paul J.
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RESULT 7
US-09-931-836-35
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-544
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APPLICANT:
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Best Local
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FILING DATE: 1999-01-22
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FILING DATE: 1998-12-15
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; NUMBER OF SEQ ID NOS: 550
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Best Local Similarity
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LENGTH: 888
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CURRENT FILING DATE: 2002-06-19
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
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PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
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ORGANISM: Homo Sapien
                                                                   869
757 RAPEQPPAPGE-PTPDGRL 774
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                               52 SVPISPVSVGRGPDPDAHV 70
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                                                                                             1 GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT 51
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                                                              GPHDLDSGLLPTPEQTPLPQKRLPTP-HPHPHALGPRAWDHGHPLLPASASSSLLLLLAPA 756
                                                                                                                                   28;
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                   Conservative
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    See File Wrapper or Palm

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Pred. No. 0.91;
7; Mismatches 33;
                                                                                                                               Score 83.5; DB Pred. No. 0.91; 7; Mismatches
                                                                                                                                                             DB 9;
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RESULT 10
US-10-176-921-544
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US-10-176-918-544
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 544
LENGTH: 888
TYPE: PRT
                                                                                                                                                                                                                                                                                                              GENERAL
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Best Local Similarity
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                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRITITLE OF INVENTION: ACII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C382
                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                             Watanabe, Colin K
                                                                               Tumas,Daniel
                                                                                             Stewart, Timothy A
                                                                                                                Smith, Victoria
                                                                                                                            Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Gurney, Austin L.
Sherwood, Steven
                                               Wood, William
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Stewart, Timothy A.
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               SECRETED AND TRANSMEMBRANE POLYPEPTIDES
ACIDS ENCODING THE SAME
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               AND NUCLEIC
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; SEQ ID NO 544
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-921-544
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US-10-036-214-35
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Best Local S
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CURRENT APPLICATION NUMBER: US/10
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See E
NUMBER OF SEQ ID NOS: 550
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APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audre
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/036,214
CURRENT FILING DATE: 2001-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
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FILING DATE: 1998-12-22
APPLICATION NUMBER: 60/113430
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                                                                                                                                                                                                                                                                                    FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/113621
FILING DATE: 1998-12-23
                               FILING DATE: 1999-03-31 APPLICATION NUMBER: 60/127706
                                                                                                                                    APPLICATION NUMBER: 60/125778
                                                                                                                                                  APPLICATION NUMBER: 60/125774 FILING DATE: 1999-03-23
                                                                                                                                                                                                   APPLICATION NUMBER: 60/116843
                                                                                                                                                                                                                    APPLICATION NUMBER: 60/115552 FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/114140 FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/113605
                 FILING DATE:
                                                                APPLICATION NUMBER:
                                                                                FILING DATE: 1999-03-
                                                                                                                 FILING DATE: 1999-03-23
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                                                                                                   APPLICATION NUMBER:
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No. US20030032061A1
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RAPPLICATION NUMBER: 60/138166

OR FILING DATE: 1999-06-08

OR APPLICATION NUMBER: 60/144791

OR FILING DATE: 1999-07-20

OR APPLICATION NUMBER: 60/146970

OR APPLICATION NUMBER: 60/146970

OR FILING DATE: 1999-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-08-25
APPLICATION NUMBER: 09/644848
FILING DATE: 2000-08-22
APPLICATION NUMBER: 09/747259
FILING DATE: 2000-12-20
                                                                              APPLICATION NUMBER: FILING DATE: 2000-12 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT,
FILING DATE: 2000-03-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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APPLICATION NUMBER: 60/132383
FILING DATE: 1999-05-04
APPLICATION NUMBER: 60/135750
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FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/132371
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APPLICATION NUMBER: 60/
FILING DATE: 1999-04-27
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                                                                                                                                    FILING DATE:
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APPLICATION
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APPLICATION NUMBER: PCT/US99/30720
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NUMBER: PCT
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US-10-137-865-544
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RESULT 13
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                                                                                                                                                                                                                                                                   Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 544
LENGTH: 888
TYPE: PRT
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SEQ ID NO 35
LENGTH: 888
TYPE: PRT
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                                                                                                                                                                          Matches
                                                                                                                                                                                                        Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C154
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PRIOR FILING DATE: 2001-07-09
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                                             757 RAPEQPPAPGE-PTPDGRL 774
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                                                                           52 SVPISPVSVGRGPDPDAHV 70
                                                                                                                                                                                      Local Similarity
                                                                                                                           52 SVPISPVSVGRGPDPDAHV 70
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                                                                                                         GPHDLDSGLLPTPEQTPLPQKRLPTP-HPHPHALGPRAWDHGHPLLPASASSSLLLLLAPA 756
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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DeForge, Laura
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b. US20030032155A1
                                                                                                                                                                        Conservative
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    See Palm or File Wrapper

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Pred. No. 0.91;
7; Mismatches
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or F:
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 544
LENGTH: 888
TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P93030R1C2
CURRENT APPLICATION NUMBER: US/10/035,719
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR APPLICATION NUMBER: 60/112514
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
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Godowski, Paul
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                                                                                                                                                                                                                                                                                                          Gurney, Austin L.
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                                                                                                                                                                                                                                                                       Stewart, Timothy A.
                                                                                                                                                                                                                                                                                            Pan, James
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Godowski, Paul J.
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    See Palm or File Wrapper

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R APPLICATION NUMBER: 09/3
R FILING DATE: 1999-05-14
R APPLICATION NUMBER: 09/31
R FILING DATE: 1999-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-03-31
APPLICATION NUMBER: 60/127706
FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/644848
FILING DATE: 2000-08-22
APPLICATION NUMBER: 09/747259
FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/132371
FILING DATE: 1999-05-04
APPLICATION NUMBER: 60/132379
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APPLICATION NUMBER: 60/114140
                 APPLICATION NUMBER: PCT/US99/28551 FILING DATE: 1999-12-02
                                                 APPLICATION NUMBER: PCT FILING DATE: 1999-05-14
                                                                                  FILING DATE:
                                                                                                  FILING DATE: 2001-0 APPLICATION NUMBER:
                                                                                                                                   FILING DATE: 2001-06-05
APPLICATION NUMBER: 09/869599
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FILING DATE: 1999-05-25
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FILING DATE: 1999-04-13
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FILING DATE: 1999-03-23
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FILING DATE: 1999-01-12
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RESULT 15
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SEQ ID NO 35
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Best Local :
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PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 93390R1C251
CURRENT APPLICATION NUMBER: US/10/142,431
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PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
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FILING DATE: 2001-06-01
APPLICATION NUMBER: PCT/US01/19692
FILING DATE: 2001-06-20
APPLICATION NUMBER: PCT/US01/21066
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FILING DATE: 2000-06-02
APPLICATION NUMBER: PCT/US00/23522
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APPLICATION NUMBER: PCT
FILING DATE: 2000-03-02
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APPLICATION NUMBER: PCT,
FILING DATE: 2000-03-01
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                                                                                                                                                                                                                                                                                                                                 Baker, Kevin P.
                                                                               Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                Zhang, Zemin
                                                                                                                                  Stewart, Timothy A
                                                                                                                                               Sherwood, Steven
Smith, Victoria
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5. US20030036179A1
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                           and is derived
                                                                                                                           Pred. No.
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1: /SIDS2/gcgdata/ge
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                                                 is the number of results predicted by chance to have a ter than or equal to the score of the result being printed. Even by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      March 4, 2003, 12:25:00; Search time 95.9157 Seconds (without alignments) 582.095 Million cell updates/sec
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                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
SUMMARIES
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419	419	419	419	419	419	419	419	419	419	ength I	
22	22	22	22	23	22	22	22	22	22	B	
AAE09210	AAE09208	AAE09181	AAE09203	AAE20348	AAE09209	AAE09207	AAE09205	AAE09212	AAE09213	ID	
P68HER-2		P68HER-2	Human p68HER-2 gen	truncate	_	Human p68HER-2 gen	Human p68HER-2 gen	Human p68HER-2 gen	Human p68HER-2 gen	Description	

ALIGNMENTS

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RESULT 1
AAE09213
ID AAE0
   /label= ECDIIIa_variant
/note= "Extracellular domain IIIa variant"
Misc-difference 124
Misc-difference 346
                      Misc-difference
                                            Misc-difference 342
                                                                                Misc-difference 125
                                                                                                                                                  Domain
                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                              HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                     15-NOV-2001
                                                                                                                                                                                                                                                                                                                           AAE09213;
                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                             Human p68HER-2 generic protein variant 11.
                                                                                                                                                                                                                                                                                                                                                 AAE09213 standard; Protein; 419
                                                                                                                                                                                                                                                                                                  (first entry)
                                                       /note= "Represented as in the specification"
                                                                                        /note= "Represented as Agn in the parent sequence shown
in the specification"
                                                                                                                                                /note= "Identical to N-terminal region of p185HER-2" 341 .419
                                                                                                                                                                       Location/Qualifiers
1..340
          .abel= Unknown
                                 abel= Unknown
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                                                                   Agn
                                                                    in the parent sequence shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel HER-2 (herstatin-2) antagonist CD particularly a polypeptide that binds to the extracellular domain (ECD) CD of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10.8. The present CD invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product CD of the alternative transcript is a truncated HER-2 protein designated CD fine alternative transcript is a truncated HER-2 protein designated CD pl85HER-2 which lacks the transmembrane and intracellular domains of pl85HER-2 but contains ECD I, II of the pl85HER-2 and the novel ECDIIIa. CT he ECDIIIa contains ECD I, II of the pl85HER-2 and thus antagonise the HER-2 receptor. The peptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify colid tumours. The present sequence is human p68HER-2 generic protein CC containing ECDIIIa variant sequence.

Note: The present sequence is not shown in the specification but is contend that the contend of the present sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide,
the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clinton G, Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence listing (AAE09181).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYOR-) UNIV OREGON HEALTH SCI.
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        121
                                                            121
                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                                                                                                                             ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                                                                                                                                          MELAALCRWGLLLALLPPGAASTQVCTGTDCKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                           402;
                                                                                                          ELTYLPTNASLSFLQDIQEVQGYVLCAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        419
                                                                                                                                                                                                                                                                                                                                           Conservative
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substituted with Leu"
356
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358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which binds to the extracellular domain of \ensuremath{\mathsf{HER}}\xspace^{-2} hard tumors -
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Pred. No. 7
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Asn"
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7.2e-169;
hes 17;
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RESULT 2
AAE09212
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                                                                                                                                                            Misc-difference 358
                                                                                                                                                                                            /label=
Misc-difference 346
                                                                                                                                                                                                                                                                               /note= "Extracellular
Misc-difference 124
                                                                                          Misc-difference
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                                                                                                                             Misc-difference 376
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                                                                                                                                                                                                                                                            Misc-difference 125
                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                          p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                HER-2; herstatin; antagonist; extracellular domestic tumour; cancer; polymorphism; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                           Human p68HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE09212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE09212 standard; Protein; 419 AA
                                        WO200161356-A1
                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XPAHPVLSFLRPSWDXVSAFYSLPLAPLDPTSVXISPVSVGRGXDPDAHVAVNLSRYEG
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                                                                                                                                                                                                                                                                                                                                                                                                           generic protein variant
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                                                         substituted with
                                                                                                                                                                                                                                                                                                               /note= "Identical to N-terminal region of p185HER-2" 341..419
                                                                                                                                                                                                                                                                   /note= "Represented as
in the specification"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /label=
                                                                 'note= "p68HER-2
                                                                                                                                                     'label=
                                                                                                                                                                                        'label= Unknown
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                                                                                 .abel= Unknown
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                                                        generic sequence (AAE09181) Xaa
Asn"
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                                                                                                                                                                                                                                                                                            variant"
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16-FEB-2001; 2001WO-US05327

23-AUG-2001

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AAE09205
ID AAEC
XX
AC AAEC
XX
DT 15-N
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CC Note: The present sequence is not shown in the specification but is contained from p68HER-2 generic sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 401
15-NOV-2001
                               AAE09205;
                                                          AAE09205 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence listing (AAE09181).
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treatment of
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                                                                                                                                                                                                                                                                        AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401;
                                                                                                                                                                                                                                                                                                                                                                                DPLXXTTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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(first entry)
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hard tumors
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95.7%;
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                                                            419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2176; DB 22;
Pred. No. 1.8e-168;
0; Mismatches 18;
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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody. Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated 968HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the specification" Misc-difference 125
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                                                                                                                                                                                                                                                                polypeptide, which binds treatment of hard tumors
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= 413
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cer; polymorphism; cytostatic; gene therapy;
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                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.

Note: The present sequence is not shown in the specification but is derived from p68HER-2 generic sequence (SEQ ID NO:2) shown in the
                                                                                                 Misc-difference
                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPVPLRMQP
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in the specification"
                                                                                                                                                                        /label= ECDIIIa_variant
/note= "Extracellular domain
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95.7%;
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DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180 DPLXXTTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA

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Misc-difference 346
                                                                                                                                                           Sequence
                                                                                                                                                                                   sequence
                                                                                                                                                                                               Note: The present sequence is not shown in the specification but is derived from p68HER-2 generic sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-2000;
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                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide, which binds treatment of hard tumors
                                                   ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                       al Similarity
400; Conserv
                                                                                                                                                                                  listing (AAE09181).
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                                                                                                         Conservative
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substituted with I
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Pred. No. 3.9e-168;
1; Mismatches 18;
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                                                                                                                              Length
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16-FEB-2001; 2001WO-US05327
                                   WO200161356
                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                     ECDIIIa; variant.
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                                                                                                                                                                                                                                                                             /note= "Identical to N-terminal region of p185HER-2" 341..419
/label= ECDIIIa_variant
/note= "Extracellular domain IIIa variant" 124
                                                                                                                                                                          /label= Unknown
356
                                                                                             substituted with
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345
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in the specification"
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10^8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p60HER-2 which lacks the transmembrane and intracellular domains of CC mreast contains ECD I. II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the ECDIIIA receptor. The peptides, which bind to an HER-2 ECD, and the cucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is human p68HER-2 generic protein CC containing ECDIIIa variant sequence.
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Best Local
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treatment of hard tumors
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95.5%;
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Protein;

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                                                                                                                                                                        The present invention relates to a method for treating a solid tumour characterised by endothelial growth factor receptor (EGFR) expression. The method involves administering an agent that binds to an extracellular domain (ECD) of EGFR. The invention also relates to a naturally occurring inhibitor of HER-2 receptor tyrosine kinase called herstatin. The co-
                                                                                                                                      expression of herstatin with p185HER2 causes a striking reduction in cell growth that corresponds with suppression of p185 autophosphorylation. The method or a pharmaceutical composition is useful for treating a solid
                                                                                                                                                                                                                                                                                Treating solid tumor characterized by expression of endothelial growth factor receptor, involves administering recombinant herstatin that binds to extracellular domain of the endothelial growth factor receptor
                                                                                                    tumour (selected from squamous cell carcinoma, lung carcinoma, colocarcinoma and glial cell tumour) characterised by EGFR expression present sequence is human truncated HER2 protein that lacks transme
                                                                                                                                                                                                                                                  Claim
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HER-2 receptor tyrosine kinase; squamous cell carcinoma; lung;
al cell tumour; cell growth.
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                        Conservative
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                                                                                                                                                                                                                                                                                                                                               Human p68HER-2 generic protein variant
                                                                                                                                                                                                                                                                                                                                                                                                        AAE09203 standard;
         Misc-difference
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                                                                                                     Misc-difference 346
                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELTYLPTNASI.SFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCVTACP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTLIDTNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                          /label=
376
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in the specification"
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                                                                                                                                                                                                                                                                   Location/Qualifiers
/label= Unknown
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                                                                                                                                                             /note= "Represented as
in the specification"
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  cytostatic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                           LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                               AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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GPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                              YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPVPLRMQP 360
                                                                                                                                                                                                                                                                                                                                                  DPLXXTTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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Pred. No. 5.7e-168;
1; Mismatches 18;
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16-FEB-2000; 2000US-0506079

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RESULT 8
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Misc-difference 361
16-FEB-2001; 2001WO-US05327
                                                                                    Misc-difference 404
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solid tumour; cancer; polymorphism; cytostatic; gene therapy;
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/note= "Encoded
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the specification"
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                              Human p68HER-2 generic protein variant 6.
                                                                                           AAE09208;
                                                                                                                        AAE09208 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids encoding these are useful to tr solid tumours. The present sequence is human containing ECDIIIa generic sequence.
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                                                             15-NOV-2001
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the treatment of hard tumors -
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                                                                                                                                                                                                 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                                                                                                                                                                                                                                                                                                                       AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                                                                                                                                                                                                         YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPVPLRMQP
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. No. 6.8e-168;
ismatches 19;
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domain;
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ECD; Herceptin;
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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of
                                         p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clinton G,
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p68HER-2; ECDIIIa; variant.
  Note: The present sequential of the present 
                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page -; 61pp; English.
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treatment of hard tumors
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solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                Human p68HER-2
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                                                                                                                                                                                                                                                                              XPAHPVLSFLRPSWDXVSAFYSLPLAPLDPTSVXISPVSVGRGXDPDAHVAVXLSRYEG
                                                                                                                                                                                                                                                                                                                 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPVPLRMQP
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346
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variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.8%;
                                                        "Represented as specification"
                                                                                                                       "Identical to N-terminal region of p185HER-2"
                                           Unknown
Unknown
                             Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2169; DB 22;
Pred. No. 6.8e-168;
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The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10~8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC MRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CP 185HER-2 and the containing ECD I. II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the notelic acids encoding these are useful to treat, diagnose and identify containing ECDIIIa variant sequence is human p68HER-2 generic protein CC containing ECDIII variant sequence.

CC Note: The present sequence.

CC Note: The present sequence is not shown in the specification but is certain decreased in the specification of the sequence listing (AAE09181).
                                                                                                                                                                                                                                                                                                                                                                                           Matches 400;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clinton G,
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Misc-difference 394
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Misc-difference 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=
Misc-difference 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2000; 2000US-0506079
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                                               181 LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                               1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide, which binds to treatment of hard tumors -
ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                         MELAALCRWGLLLALLPPGAASTQVCTGTDCKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                         ELTYLPTNASLSFLQDIQEVQGYVLCAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Score 2169; DB 22;
Pred. No. 6.8e-168;
0; Mismatches 19;
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solid tumour; can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human p68HER-2 generic protein variant
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                      (UYOR-) UNIV OREGON HEALTH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECDIIIa; variant.
                                                                                                          2001WO-US05327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tin; antagonist; extracellular domain; ECD; Herceptin;
cancer; polymorphism; cytostatic; gene therapy;
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substituted with G
e 358
                                                                                                                                                                                                                                                             /label= Unknown
413
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/note= "Extraceilular domain IIIa variant"
124
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376
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in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CP 185HER-2 but containing ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is human p68HER-2 generic protein CC containing ECDIIIa variant sequence.

CC Note: The present sequence is not shown in the specification but is CC derived from p68HER-2 generic sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELAALCRWGLLLALLPPGAASTQVCTGTDCKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400;
                                                                                                                                                                                                                                                                                                                                                        LTLIDTNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                              419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2168; DB 22;
Pred. No. 8.2e-168;
0; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extracellular domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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HER-2; herstatin; antagonist; extracellular

Human p68HER-2 generic protein

variant

9

domain;

ECD; Herceptin;

15-NOV-2001

(first entry)

solid

0;

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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIII a variant sequence.
solid tumours. The present sequence is human containing ECDIIIa variant sequence.

Note: The present sequence is not shown in the
                                                                                                                                                                                                                                                                                                       Clinton G,
                                                                                                                                                                                                            Example 11; Page -; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                 (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                           16-FEB-2000; 2000US-0506079.
                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-2001; 2001WO-US05327
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                                                                                                                                                                                                                                      polypeptide,
treatment of
                                                                                                                                                                                                                                                                                                       Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "p68HER-2 (
substituted with I
s 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                      which binds to hard tumors -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= ECDIIIa_variant
/note= "Extracellular d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Identical to N-terminal region 341..419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
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in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
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                                                                                                                                                                                                                                                                                                       Evans
                                                                                                                                                                                                                                                   the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           generic sequence (AAE09181) Xaa
Leu"
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specification but
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                                                                                                                                                                                                                                                   of HER-2
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RESULT 13
AAE09204
ID AAE09
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                                                                                                                   /label= ECDIIIa_variant
/note= "Extracellular domain IIIa variant"
Misc-difference 124
          Misc-difference
                                        Misc-difference
                                                                                          Misc-difference
                                                                                                                                                       Domain
                                                                                                                                                                                    Key
                                                                                                                                                                                                                                    HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                 AAE09204 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived from p68HER-2 generic sequence (SEQ ID NO:2) sequence listing (AAE09181).
                                                            Misc-difference
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                          15-NOV-2001
                                                                                                                                                                                                                                                                                                               AAE09204;
                                                                                                                                                                          Region
                                                                                                                                                                                                                            р68нЕR-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                                                                    XPAHPVLSFLRPSWDXVSAFYSLPLAPLDPTSVXISPVSVGRGLDPDAHVAVXLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                               GPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                       YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPVPLRMQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPLXXTTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCTGFKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                                                                                                                                                                                                                                                                                                                                                                                                                             YNKLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGXHSXXPRPAAVPVPXRXQP
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                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                      generic
        /note= "p68HER-2 substituted with 346
                                         345
                                                             342
                                                                                          125
                                                                    /note= "Represented as in the specification"
                                                                                                                                                      /note= "Identical to N-terminal region of p185HER-2" 341..419
                                                                                                                                                                          Location/Qualifiers
1..340
/label= Unknowr
                                                                                                               /note=
                                                 'label=
                                                                                                    the
                                                                                                                                                                                                                             variant
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                                                                                         specification"
                                                                                                                                                                                                                                                                    protein variant
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                                                 Unknown
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Pred. No. 8.2e
0; Mismatches
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                   generic
Pro"
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8.2e-168;
nes 19;
                             sequence (AAE09181)
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                                                                               parent sequence
                                                                                                             parent sequence
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                                                                                                                                                                                                                                                                                   The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised cantibody, Herceptin, at an affinity of at least 10°8: The present CI invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated CC p88HER-2 which lacks the transmembrane and intracellular domains of CP 185HER-2 but containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the culcic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein CC Note: The present sequence is now in the specification but is containing ECDIII variant sequence.

Note: The present sequence (SEQ ID NO:2) shown in the containing (AAE09181).
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-2001; 2001WO-US05327
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                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYOR-) UNIV OREGON HEALTH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide, which binds to treatment of hard tumors -
                                                                                                                                                     400;
             LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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LTLIDTNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                 DPLXXTTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                               DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                                                                  ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                     ELTYLPTNASLSFLQDIQEVQGYVLCAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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و
                                                                                                                                                                                                                                                               419 AA;
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                                                                                                                                                                                                                         94.8%;
95.5%;
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                                                                                                                                                                                                          Score 2167; D
Pred. No. 9.9e
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                                                                                                                                                                                                          DB 22;
).9e-168;
hes 19;
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RESULT 14
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/note= "Represented
the specification"
Misc-difference 125
                                                                                                                                                                                      Misc-difference 345
                                                                                                                                                                                                the specification Misc-difference 342
                                                   Misc-difference
                                                                Misc-difference
                                                                             Misc-difference
                                                                                          /Id
Misc-difference 376
                                                                                                        Misc-difference
                                                                                                                      Misc-difference
                                                                                                                                   Misc-difference
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                                                                                                                                                            Misc-difference
                                                                                                                                                                         Misc-difference 346
                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                           p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                     Human p68HER-2 generic protein variant 15.
                                                                                                                                                                                                                                                                                                                                                                AAE09216;
                                                                                                                                                                                                                                                                                                                                                                             AAE09216 standard;
                         WO200161356-A1
                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                              Homo sapiens.
            23-AUG-2001
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tumour; can
                                                                                                                                                                                                                                                                                                                  cancer;
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357
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                                      /note= "p68HER-2 generic sequence (AAE09183) Xaa substituted with Asn"
                                                                                                                                                                                                                                                              /note= "Identical to N-terminal region 341...419
                                                                                                                                                                                                                                                /label= ECDIIIa_variant
/note= "Extracellular d
                                                                                     /label=
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                         'label=
                                                                                                                                                                                                                                                                                                                      antagonist; extracellular domain; ECD; Herceptin;
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                                                                                                                                                                                                                                   sequence shown
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16-FEB-2001; 2001WO-US05327

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RESULT 15
AAE09200
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AC AAEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10^8. The present cinvention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated CC p6HER-2 which lacks the transmembrane and intracellular domains of CP HESHER-2 which lacks the transmembrane and intracellular domains of CP HESHER-2 which lacks the transmembrane and intracellular domains of CC containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the culties encoding these are useful to treat, diagnose and identify containing ECDIII a variant sequence is human p68HER-2 generic protein CC containing ECDIII a variant sequence.

CC Note: The present sequence is not shown in the specification but is derived from p68HER-2 generic sequence (SEQ ID NO:13) shown in the containing (AAEO9183).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                AAE09200 standard;
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                                                                                                                                                     GPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                          YNYLSTDYGSCTLYCPLHNQEYTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPYPLRMQP
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                                                                                                                                     XPAHPVLSFLXPSWDXVSAFYSLPLAPLDPTSVXISPVSVGRGXDPDAHVAVNLSRYEG
                                                                                                                                                                                                        YNKLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGXHSXXPRPAAVPVPXXXQP
                                                                                                                                                                                                                                                                         AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                           AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                                                                                                                                                                                                                                                                                                                               LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                  Protein;
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Pred. No. 1.7e-167;
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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of
                                                                                           Example 12; Page -;
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solid tumour; cancer; polymor]
                                                                                                                                                                                     (UYOR-) UNIV OREGON HEALTH SCI
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                                                                                                               polypeptide, which binds to treatment of hard tumors -
                                                                                                                                              2001-529934/58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECDIIIa; variant.
                                                                                                                                                                Henner WD,
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357
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358
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/note= "Extracellular domain
124
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356
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tuted with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identical to N-terminal region of p185HER-2"
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Search completed: March Job time: 97.9157 secs
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Best Local Similarity
Matches 399; Conserv
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Note: The present sequence is not shown in the specification but is derived from p68HER-2 generic sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence listing (AAE09181).
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                       YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPVPLRMQP 360
                                                                                                                                                                                                                                                        LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                                                                                                                                                                                                                                                                                                                     DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
              4, 2003, 12:34:33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2161; DB 22; Length 419;
Pred. No. 3e-167;
0; Mismatches 20; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                         240
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14)

OM protein - protein search, using sw model GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

March 4, 2003, 12:31:51; Search time 24.3996 Seconds (without alignments) 1650.860 Million cell updates/sec

Run on:

Title: Perfect score: Sequence: US-09-234-208B-2 2287 1 MELAALCRWGLLLALLPPGA.....VGRGPDPDAHVAVNLSRYEG 419

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21					16	15	14				10	9	8	7	O	ر د		ω	2 1	_	No.	Result
263.5		272	278	291	294	294	331	33		363.5	363.5	415	416	419	419	575.5	681.5	692	735.5	775	781.5	789	793	794	796.5	1571	1608.5	1878	Score	
11.5	11.8	11.9		12.7				14.5			•		٠				•				•	•	•	34.7			70.3	2.	Match	* Query
1382	1607	540	1300	1477	2148	2101	342	333	1363	1717	366	1330	1369	1374	1323	843	1166	1339	1342	1308	644	1210	1210	527	1223	1254	1260	1255	Length	
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insulin receptor p		receptor-	receptor-	•		O	epidermal growth f	epidermal growth f	insulin-like growt	growt	growth	epidermal growth f	protein-tyrosine k	Ō	protein let-23 (im	epidermal growth f	yrosine		lated tr	l growth	l growth	1 growth	growth		idermal growth	precursor -	in-tyrosine	ein-tyro	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
131.5	132	133.5	136.5	142	144	160.5	203	226.5	235	249	252.5	257.5	258	261	263.5
5.7	5. 8	5. 8	6.0	6.2	6.3	7.0	8.9	9.9	10.3	10.9	11.0	11.3	11.3	11.4	11.5
915	1574	915	1111	1959	1548	1299	1846	183	329	1268	1371	1367	1390	1372	1383
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B48225	T13954	A48225	T26972	AGRT	S34583	T43251	T42047	JH0803	A48805	в36502	A33837	IGHUR1	T30346	A34157	A36080
probable proprotei	MEGF6 protein - ra	subtilisin-like pr	hypothetical prote	agrin - rat	serine proteinase	furin (EC 3.4.21.7	insulin receptor h	tyrosine kinase re	insulin-like growt	insulin receptor-r	insulin-like growt	insulin-like growt	insulin receptor -	insulin receptor p	insulin receptor p

ALIGNMENTS

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F;1-21/Domain: s
F;22-1255/Produc
F;22-653/Domain:
F;70-304/Domain:
     Nature 3
A; Title:
                       protein-tyrosine kinase (EC 2.7.1.112) neu precursor C:Sepecies: Rattus norvegicus (Norway rat) C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #t C:Accession: A24562; A61204 R:Bargmann, C:I.; Hung, M.C.; Weinberg, R.A. Nature 319, 226-230, 1986
                                                                                                                                                                                                     RESULT
TVRTNU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332 C;Comment: Amplification and overexpression of this erbB-related gene occurs in C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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A;Cross-references:
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Matches 362
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;718-983/Domain: protein kinase homology <KIN>
;718-734/Region: protein kinase homology <KIN>
;726-734/Region: protein kinase AFP-binding for the contif for the continuous for the co
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;22-637/Domain: extracellular #status predicted <EXT>
;70-304/Domain: Egf receptor extracellular domain repeat <EE1>;395-605/Domain: Egf receptor extracellular domain repeat <EE2;654-675/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                              --PDAHVAVNLSRYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----
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GDB:120613;
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83.0%;
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Pred. No. 5
epidermal
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5.9e-121;
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A; Residues: 1-1254 <R
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                                                                                                             A; Accession: I48161
                                                                                                                                          A; Reference number: I48161;
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A; Cross-references:
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A; Molecule type: DNA
A; Residues: 637-663,'V',665-702 <MAS>
A; Residues: 637-663,'V',665-702 <MAS>
A; Residues: 637-663,'V',665-702 <MAS>
A; Rote: authors translated the codon GCA for residue 25 as Val
C; Genetics:
C; Genetics:
C; Genetics:
A; Gene: neu
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; protein-tyrosine kinase neu *status predicted <MAT>
F; 1-19/Domain: signal sequence *status predicted <TMN>
F; 20-1260/Product: protein-tyrosine kinase neu *status predicted <MAT>
F; 658-680/Domain: protein kinase homology <KIN>
F; 731-739/Region: protein kinase ATP-binding motif
F; 71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) *status predicted
F; 691/Binding site: phosphate (Thr) (covalent) *status predicted
F; 682,1227,1253/Binding site: phosphate (Tyr) (covalent) *status predicted
                                                                                                         p-185 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
                     Gene 140, 251-255, 19
A; Title: Cloning and
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A:Accession: A61204
A:Status: preliminary
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A;Accession: A244562
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Residues: 1-1260 <BAR>
A;Cross references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R;Masul. T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith
Carcinogenesis 12, 1975-1978, 1991
                                                                   R;Nakamura,
                                                                                           C; Accession:
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                                                                   T.; Ushijima,
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                     activation of
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                                                                   T.; Ishizaka, Y.;
MUID:94193007; PMID:79082
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                                                                   Nagao, M.;
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                                                                   M.; Yamazaki,
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GB:D16295;

NID:g493236;

PIDN:BAA03801.1;

PID: 9747595

translated

from

GB/EMBL/DDBJ

PMID:7908275

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Mar

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epidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Gallus gallus (chicken)
C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; A00643
R;Lax, I; Johnson, A.; Howk, R; Sap, J; Bellot, F; Winkler, M.; Ullrich, A.;
Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression
A;Reference number: A27720; MUID:88261272; PMID:3260329
A;Accession: A27720
A;Molecule type: mRNA
A;Residues: 1-1223 <LAX>
A;Cross-references: GB:M20386
R:Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Ra
Cell 41, 719-726, 1985
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing
A;Reference number: A00643; MUID:8528222; PMID:2988784
A;Residues: 585-1223 <NIL>
A;Cross-references: GB:M10066
C;Genetics:
A;Gene: erbB
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics: alternative splicing; AfP; autophosphorylation; glycoprotein; growth
Decific protein kinase
pecific protein kinase F;1-30/Domain: signal se F;31-1223/Product: epide F;31-654/Domain: extrace F;81-307/Domain: EGF ree F;397-610/Domain: EGF re
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A;Gene: neu
C;Superfamily: epidermal gru
C;Keywords: ATP
F;718-983/Domain: protein k
F;726-734/Region: protein k
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;1-30/Domain: signal sequence #status predicted <SIG>;31-123/Product: epidermal growth factor receptor #status;31-1654/Domain: extracellular #status predicted <EXT>;81-307/Domain: EGF receptor extracellular domain repeat <E;397-610/Domain: EGF receptor extracellular domain repeat <
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kinase ATP-binding
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pred. No. 6.7;
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C;Date: J. J. C;Accession: A42032
C;Accession: A42032
R;Flickinger, T.W.; Maihle, N.J.; Kung, H.J.
Mol. Cell. Biol. 12, 883-893, 1992
Mol. Cell. Biol. 12, 883-893, 1992
A;Title: An alternatively processed mRNA from the avian
A;Title: An alternatively processed mRNA from the avian
A;Title: An alternatively processed mRNA from the avian
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F;7719-984/Domain: protein kinase homology <KIN>
F;719-984/Domain: protein kinase homology <KIN>
F;727-735/Region: protein kinase ATP-binding motif
F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent)
F;192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte
F;754/Active site: Lys #status predicted
F;754/Active site: Lys #status predicted
F;7100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #s
                                                                                                                                                                                                                                                                                                                        A;Note: sequence extracted from NCBI backbone (NCBIN:76892, NCBIP:76893) C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epidermal growth factor receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
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A; Residues: 1-527 <FLI>
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                                                                                                                                                                                             LLLALLPPGAAST-----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYL 65
                                                                                         PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNN 125
                                                                  EHNRDLTFLKTIQEVAGYVLIALNMVDVIPLENLQIIRGNVLYDNSFALAVLSNYH-MNK
                                                                                                                                                     LLLLLGRVALCSAVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLEITYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHNYVVTDHGSCVRSCNTDTYEV-EENGVRKCKKCDGLCSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RWGLLLALLPPGAA-----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE
                                                                                                                                                                                                                                          155;
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                           34.7%;
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                                                                                                                                                                                                                                     Score 794; DB
Pred. No. 4.6e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 7.66
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 796.5;
Pred. No. 7.
                                                                                                                                                                                                                                                     4; DB 2;
. 4.6e-47;
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hes 112;
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A;Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfl.
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A;Title: The human EGF receptor gene: structure of the 110 kb locus and iden
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A;Accession: S30024
A;Molecule type: DNA
A;Residues: 1-29 <HA2>
A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R;Haley, J.D.; Waterfield, M.D.
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A;Title: Contributory effects of de Novo transcription and premature transcr
A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Residues: 1-29 <HAL>
                                                                                                                                                      A;Cross references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A;Experimental source: carcinoma cell line A431-7
R;Xu, Y; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Mer Nature 309, 806-810, 1984
A;Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs A;Reference number: A00642; MUID:84245835; PMID:6330563
A;Recession: A00642
A;Molecule type: mRNA
A;Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321
A;Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-321
A;Perimental source: A431 human carcinoma cells, which have large numbers of EGF receptors and the surface of 
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A;Accession: A00641
A;Molecule type; mRNA
A;Residues: 1-1210 <ULL>
A;Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924
A;Note: the authors translated the codon AAG for residue 540 as Asn
R;Ishil, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the humar
A;Reference number: A25772
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <ISH>
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A;Title: Expression cloning of human EGF receptor complementary DNA: R:Reference number: A43615; MUID:84196372; PMID:6326261 A;Accession: A43615 A;Accession: A43615 A;Molecule type: mRNA
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Science 224, 294-297,
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A; Residues: 1028-1210
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297, 1984
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A.Title: Functional independence of the epidermal growth factor r A.Title: Functional independence of the epidermal growth factor r A.Contents: annotation; internalization signal C.Comment: Binding of EGF to the receptor leads to internalizatio c.Genetics: A.Gene: GDB:EGFR A.Ge
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A; Molecule type: protein
A; Residues: 25-30, 's', 32-51; 454-467 <WEB>
A; Residues: 25-30, 's', 32-51; 454-467 <WEB>
A; Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros
J. Biol. Chem. 260, 5205-5208, 1985
A; Title: Identification of residues in the number: A60143; MUID: 85182650; PM
A; Reference number: A60143; MUID: 85182650; PM
A; Accession: A60143
A; Molecule type: protein
A; Residues: 740-744, 'X', 746-747 <RUS>
R; Mroczkowski, B; Mosig, G.; Cohen, S.
Nature 309, 270-273, 1984
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A;Reference number: anotation; receptor activity
A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DN R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; De Cell 59, 33-43, 1989
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Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23067. MITTO. 0260127132, 1984
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11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
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epidermal growth factor receptor precursor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, Genes Dev, 8, 399-413, 1994
A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF rece A;Reference number: A53183; MUID:94170986; PMID:8125255
A;Molecule type: mRNA
A;Residues: 1-1210 CLUE>
A;Reference number: A53183
                                                                                                                            C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; growth factor receptor; kinase-related transforming pro F;1-24/Domain: signal sequence #status predicted <SIG> F;648-670/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 12-20,22-132 <RES>
A;Cross-references: GB:L06864; NID:g193001; PIDN:AAA53029.1; PID:g567201
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A;Title: Expression of the epidermal growth factor receptor ger A;Reference number: I49643; MUID:93126380; PMID:7678348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Molecule type: protein
A:Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009,
R:Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
A:Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor A;Reference number: $45325
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A: Residues: 1-714 < AVI>
A: Cross-references: GB: X59698
R: Elsinger, D.P.; Serrero, G.
submitted to the EMBL Data Library,
      F;711-977/Domain: protein kinase homology <KIN>F;712-728/Region: protein kinase ATP-binding motif F;680,695/Binding site: phosphate (Thr) (covalent) F;697,1070,1071/Binding site: phosphate (Ser) (covalent)
                                                                                                                                                                                                  A;Gene: EGFR
C;Superfamily: e
C;Keywords: ATP;
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R;Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
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R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger,
Oncogene 6, 673-676, 1991
A;Title: Comparison of EGF receptor sequences as
A;Reference number: A43818; MUID:91232866; PMID:2
A;Accession: A43818
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A; Residues: 1-971, 'K', 973-1210 <VER>
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A; Residues: 969-971, 'K', 973-1115, 'D'
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PMID:2030916
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Ş 망 Qy 밁 ρy В δÃ F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status ex F;1197/Binding site: phosphate (Tyr) (covalent) #status experimental experimenta

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RESULT
A36325
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                                                                                                                                                                                                                                                                                                                                                                                                                             11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                    LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR
                                                                                                                                                                                                                                                                                                                                                ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                                                                                                                                                               VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRK
                                                                                                                               CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY
                                                                                                                                                             CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                              -YGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL---
                                                                                                                                                                                                                                                                                              VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI 184
                                                                                                                                                                                                                                                                                                                             YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN------
                                                                                                                                                                                                                                                                                                                                                                                              LLTALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRN
                                                                                                                                                                                              -QSHPSSCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 789; DB 2;
Pred. No. 2.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 116;
                                                                                            340
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Ωy

DЬ Qy

B

C:Species: Rattus norvegicus (Norway ro C:Date: 25-Jan-1991 #sequence_revision C:Accession: A36325 C; Keywords: alternative splicing; A;Cross-references: GB:M37394 C;Superfamily: epidermal growth factor receptor; protein kinase homology A; Residues: 1-644 <PET> A; Status: preliminary A; Reference number: A36325; A; Accession: A36325 epidermal growth factor receptor - rat
C; Species: Rattus norvegicus (Norway r A; Molecule type: mRNA A; Title: A truncated, Mol. R; Petch, L.A.; Query Match Best Local Matches Cell. Biol. Similarity Harris, 10, Conservative s, J.; Raymond, 2973-2982, 199 secreted form 34.2%; ted form of the MUID:90258888; 44; 1990 ATP; growth factor receptor Pred. Score 781.5; V.W.; Blasband, Mismatches 25-Jan-1991 #text_change 10-Oct-1997 No. 4.1e-46 epidermal growth PMID:2342466 DB 2; 117; Α., Length Indels Lee, factor D.C.; 644; 23; receptor is Earp, H.S. Gaps 7; encode

В

125 122

Qy В δÃ В Qy

PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL 181

----YGTNKTGLRELPMRNLQEILIGAVRFSNNPILCNMETIQWRDIV-QDVFLSN

175

235 239

299

TLIDTNRS-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ

LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD 121

67 62 15

3 LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE 61

LAALCAAG-----GALEEKKYCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE

66

Š В Ωy

240 176

CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC MSMDVQRHLTGCPKCDPSCPNGSCWGRGEENCQKLTKIICAQQCSRRCRGRSPSDCCHNQ

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C;Accession: A36223; I59164
R;Kraus, M.H.; Issing, W.; Miki, T.; Popeso
Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197
A;Title: Isolation and characterization of
A;Reference number: A36223; MUID:90083234;
A;Accession: A36223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Residues: 1-1308 <PLO>
A:Cross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A:Cross-references: GB:L07868; NID:g337359; PIDN:AAB59446.1; PID:g337360
A:Note: sequence extracted from NCBI backbone (NCBIP:126042)
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; growth factor receptor
F:716-981/Domain: protein kinase homology <KIN>
F:724-732/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993
A; Title: Ligand-specific activation of HER4/p180erb84, a A; Reference number: A47253; MUID:93189574; PMID:8383326
A; Accession: A47253
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C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: A47253
                 A; Molecule type: mRNA
A; Residues: 1-1342 <KRA>
A; Cross-references: GB:M29366
                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 17-Nov-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth C; Species: Homo s
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                                                                                                                                                                                                                                                                                                                                 V-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLM
                                                                                                                                                                                                                                                                                                                                                                     LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGLLLALLPPGAA----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRNYVVTDHGSCVRACGPDYYEV-EEDGVSKCKKCDGPCRK 335
                                                                                                                                                                                                                                                                                                                                                                                                        CSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTFQLEHNFNAKYTYGAFCVKKCPHNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STNGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPYVSDCCHRECAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTNRSRACHPCSPMCKGSRCWGESSEDCOSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NF-----GLQELGLKNLTEILNGGVYVDQNKFLCYADTIHWQDIVRNPWPSNLTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEHNRDLSFLRSVREVTGYVLVALNQFRYLPLENLRIIRGTKLYEDRYALAIFLNYRKDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVWVSLLVAAGTVQPSDSQSVCAGTENKLSSLSDLEQQYRALRKYYENCEVVMGNLEITS
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 G.D.;
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Whitney,
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 G.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
Neubauer,
                                                                                                                                              T.; Popescu, N.C.; 9193-9197, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 775; Db 2,
No. 2.4e-45;
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 M.G.;
                                                                                                            ERBB3, a thi:
PMID:2687875
                                                                                                                                                                                                                                      (EC 2.7.1.-)
 Green,
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                                                                                                                               a third
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                                                                                                                                                               Aaronson,
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 McDonald, V.L.;
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                                                                                                                             ERBB/epidermal
 Todaro,
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 G
F;705-970/Domain:
F;713-721/Region:
                                                                                                                                                                                                    A; Experimental source: liver
                                                                                                                                                                                                                                                                          A; Title: Cloning of the rat A; Reference number: JC4387; A; Accession: JC4387
                                                                                                                                                                                                                                                                                                                               R;Hellyer, N.J.; Kim, H.H.;
Gene 165, 279-284, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150;
                 protein
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A;Map position: 12q13-12q13
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C;Keywords: ATP; phosphotransferase
E;707-972/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: mRNA
A:Residues: 1-559,'G',561-957,'F',959-1063,'G',1065-1342 •
A:Cross-references: GB:M34309; NID:g183990; PIDN:AAA355979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 87, 4905-4909, 1990
A;Title: Molecular cloning and expression of another epidermal growth factor receptor A;Reference number: I59164; MUID:90311312; PMID:2164210
A;Accession: I59164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;707-972/Domain: protein kinase homology <K: F;715-723/Region: protein kinase ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GDB:119880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
                                                                                                                                                                                                                 DQTSCVRACPPDKMEVD-KNGLKMCEPCGGLCPKACEGTGS 336
                                                DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR---GTHS
                                                                                                                                                                                                                                                                     RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG
                                                                                                                                                                                                                                                                                                                           ----NSSHALRQLRLTQLTEILSGGYYIEKNDKLCHMDTIDWRDIVRDRD----AEIVVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
                                                                                                       PQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFV-V
                                                                                                                                                          PKHSDCLACLHENHSGICELHCPALVIYNTDTFESMPNPEGRYTFGASCVTACPYNYLST 306
                                                                                                                                                                                                                                                                                                                                                                               PVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                     NADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVM-----LNYNT
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Pred. No. 1.3e-42;
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A,Gene: ErbB3:
A,Gene A;Note: The authors translated the codon AAC for residue 30 C;Comment: This protein is a functional heregulin receptor C;Genetics: N, Alternaté names: ErbB3 protein; HER3 protein; C;Species: Rattus norvegicus (Norway rat) C;Date: 17-Jan-1996 #sequence_revision 19 C;Accession: JC4387 F;20-1339/Product: epidermal growth factor homolog #sta F;640-659/Domain: transmembrane #status predicted <TMM> A;Molecule type: mRNA
A;Residues: 1-1339 <HEL>
A;Cross-references: GB:U29339; NID:g915389; growth factor receptor homolog precursor kinase homology <KIN> ErbB3 cDNA and MUID:96096535; Greaves, C.H.; 19-Apr-1996 protein characterization of the recombinant $\ensuremath{\mathsf{PMID}}\xspace:8522190$ Sierke, PID:g915390 S.L.; #text_change 369 as or that Koland, J.G predicted Thr and GT transduces 13-Nov-1998 transmembrane protein kinase <MAT> GTT

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A;Accession. ...
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X16891; NID:g65290;
A;Cross-references: EMBL:X16891; NID:g65290;
A;Cross-references: EMBL:X16891; NID:g65290;
A;Cross-references: EMBL:X16891; NID:g65290;
                                                                                                                                                 A:Map position: Y
A:Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A:Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C:Superfamily: epidermal growth factor receptor; prosphotransferase; transmembrane F:1-25/Domain: signal sequence #status predicted <SIG>F:26-1166/Product: kinase-related transforming protein (Tu) #status predict F:707-972/Domain: protein kinase homology <KIN>F:715-723/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish N;Alternate names: epidermal growth factor receptor homolog; kinase-related C;Species: Xiphophorus maculatus (southern platyfish) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 C;Accession: S06142; S13809
R;Wittbrodt, J.; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, Nature 341, 415-421, 1989
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                                     Qy
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A;Molecule type: DNA
A;Residues: 821-1025,'N',1027-1098,'A',1100-1166 <ADA>
A;Cross-references: EMBL:X56319; NID:g65284; PIDN:CAA39763.1; PID:g65285
                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 6, 73-80, 1991
A; Title: Transcriptional activation of the melanoma inducing A; Reference number: $13807; MUID:91125882; PMID:1846957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-inducing A;Reference number: S06142; MUID:90015140; PMID:2797166 A;Accession: S06142
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                                                                                                 Query Match
Best Local Similarity
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                                     AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPHNFV-VDQTFCVRACPPDKMEVD-KHGLKMCEPCGGLCPKACEGTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR---GTHS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAEIVVKNNGANCPPCHEVCKG-RCWGPGPDDCQILTKTICAPQCNGRCFGPNPNQCCHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119
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   AALLQ--LLLVLSISRCCSTDPDRKVCQGTSNQMTM----LDNHYLKMKKMYSGCNVVLEN
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Pred. No. 1.2e-39;
                                                                                               Score 681.5; DB 1;
Pred. No. 5.5e-39;
                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA34770.1;
                                                                             136;
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R:Schejter, E.D.; Segal, D.;
Cell 46, 1091-1101, 1986
A;Title: Alternative 5' exor
A;Reference number: A27131,
A;Accession: A27131
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C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epidermal growth factor receptor - fruit fly (Drosophila melanogaster) (fra c;Species: Drosophila melanogaster C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-May-1997 C;Accession: A27131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-843 < SCH>
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                                                                                                                                                                                                                                               YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE 214
                                                                                                                                                                                                                                                                                        RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP 197
                                                                                                                                                                                                                                                                                                                                    YILISHVDVKKVVFPKLQIIRGRTLFSLSVEEEKYALFV--
                                                                                                                                                                                                                                                                                                                                                                         YVLIAHNQVRQVPLQRLRIVRGTQLF-----EDNYALAVLDNGDPLNNTTPVTGASPGGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPK 339
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                                                                                KNFFDEAVSKEECPPMRKYNPTTYVLETNPEGKYAYGATCVKECP-GHLLRDNGACVRSC
                                                                                                                     LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
                                                                                                                                                              SCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC
                                                                                                                                                                                                        MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
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119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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CVPCNGPCPK
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36.6%;
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Pred. No. 7.2e-32;
352
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let-23

[imported] -

Caenorhabditis elegans

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C;Species: Caenorhabdit;
C;Date: 10-May-2001 #sec
C;Date: 10-May-2001 #se
C;Accession: E88257
R;anonymous, The C. elec
Science 282, 2012-2018,
                                                                                                                                                                                                                                                                                                                       protein-tyrosine kinase (EC 2.7.1.112) let-23 precursor %,Alternate names: receptor tyrosine kinase let-23 C;Species: Caenorhabditis elegans C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text C;Accession: S70712; S73101; S13422; T27682 R;Sakai T; Koga, M; Ohshina, Y. J. Koga, M; Ohshina, Y. J. Mol. Biol. 256, 548-555, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Genome sequence of the nematode C. elegans: a | A:Reference number: A75000; MUID:99069613; PMID:9851916 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ ann A:Note: published errata appeared in Science 283, 35, 1:A:Accession: E88257
                                                                                                                                                                                                                                                       A; Reference number: S70712; MUID:96177760; PMID:8604137 A; Accession: S70712
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A;Map position:
C;Superfamily: u
A; Molecule type: DNA
A; Residues: 1-50, 'G', 52-1374 < KOG>
A; Cross-references: EMBL.D63426; N
A; Experimental source: strain N2
                                                                                                    submitted to the EMBL Data A; Reference number: S73101
                                                                                                                                          R; Koga,
                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1374 <SAK>
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                                                                                                                                                                 A; Experimental source: strain
                                                                                                                                                                                 Cross-references: EMBL:D63426
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                                                                                 Accession: S73101
                                                                                                                                                                                                                                                Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNHCVKECPPELLIENDV--CVRHCSDGHHYDATKD--VRECEKCRSSSCPK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GASCYTACPYNYL-STDYGSCTLYC-PLHNQEYTAEDGTQRCEKC-SKPCAR 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYECCDSACLGGCTGHGPKNCIACSKYELDGICIETCPSRKIFNHKTGRLVFNPDGRYQN
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018, 1998
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                       NID:g1407562;
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Pred. No. 6.1e-21;
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                                                                                                                           1995
                       PIDN:BAA09729.1;
                                                                                                                                                                                                                                                                                                                                                                                    #text_change 11-Jan-2002
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, 1999; Science 283, 2103, 1999; an
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                       PID:g1407563
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A;Map position: 2
A;Introns: 44/1; 51/1; 90/1; 112/3; 165/3; 217/1; 290/1; 379/1; 418/1; 448/2; 565/1;
A;Introns: 44/1; 51/1; 90/1; 112/3; 165/3; 217/1; 290/1; 379/1; 418/1; 448/2; 565/1;
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinases; protein c;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein F;1-28/Domain; signal sequence #status predicted <SIG> F;29-1374/Product: protein-tyrosine kinase let-23 #status predicted <MAT> F;942-950/Region: protein kinase homology <KIN> F;942-950/Region: protein kinase ATP-binding motif
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A;Titite: The let-23 gene necessary for Caenorhabditis elegans vulval induction A;Reference number: S13422; MUID:91080919; PMID:1979659
A;Accession: S13422
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A;Experimental source: clone ZK1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 52-1374 <WIL>
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A; Residues: 52-1374 < ARO>
В
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                                             292 GASCVTACPYNYL-STDVGSCTLVC-PLHNQEVTAEDGTQRCEKC-SKPCAR
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                                                                                                SYECCDSACLGGCTGHGPKNCIACSKYELDGICIETCPSRKIFNHKTGRLVFNPDGRYQN
                                                                                                                                                                                                                                           TLIDTNRSRACH-----PCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARC---KGPL
                                                                                                                                                                                                                                                                                                                                      LNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCY-QDTILWKDIFHKNNQLAL 181
  GNHCVKECPPELLIENDV - - CVRHCSDGHHYDATKD - - VRECEKCRSSSCPK
                                                                                                                                           PTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTF
                                                                                                                                                                                             KVETTNSHQHCYQNGKSMAKCHESC-NDKCWGSGDNDCQRVYRSVCPKSCSQCFYSNSTS
                                                                                                                                                                                                                                                                                                                                                                                        NEDSPLKSINFFONLEEIRGSLIIYRANIQKISFPRLRVIYGDEVFHDN-ALYIHKNDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP 122
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Pred. No. 6.4e-21;
9; Mismatches 131
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Search completed: March 4, 2003, 12:36:37 Job time: 27.3996 secs

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Title:
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                                                                                  Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5
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                                          112892 seqs, 41476328 residues
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2287
1 MELAALCRWGLLLALLPPGA.....VGRGPDPDAHVAVNLSRYEG 419
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES .

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ALIGNMENTS

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VARIANTS VAL-654 AND VAL-655. MEDLINE=93194196; PubMed=8095488; Ehsani A., Low J., Wallace R.B., Wu A.M.; Characterization of a new allele of the human ERBB2 gene by allele-specific competition hybridization."; Genomics 15:426-429(1993). -i- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, -ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF- ALPHA AND AMPHIREGULIN. -i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphatei- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS (POTENTIAL). -i- SUBCELLULAR LOCATION: Type I membrane protein.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=86070181; PubMed=2999974; Coussens L., Yang-Feng T.L., Libermann T.A., Schlessinger J., McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J., McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J., Francke U., Levinson A., Ullrich A.; "Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with neu oncogene."; Science 230:1132-1139(1985). [3] SEQUENCE OF 737-1031 FROM N.A. MEDLINE=86016729; PubMed=2995967; Semba K., Kamata N., Toyoshima K., Yamamoto T.; Semba K., Kamata N., Toyoshima K., Yamamoto T.; Pa v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a human salivary gland adenocarcinoma."; Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=86118663; PubMed=3003577; Yamamoto T., Tkawa S., Akiyama T., Semba K., Nomura N., Miyajima N., Saito T., Toyoshima K.; "Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor."; Nature 319:230-234(1986).	LT 1 HUMAN ERB2_HUMAN P04626; 13-AUG-1987 (13-AUG-1987 (13-JUN-2002 (Receptor prot (p185erb82 or HER2 ERBB2 OR HER2

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Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2
Pfam; PF02757; YLP; 2.
Pfam; PF0000001; Euk_pkinase; 1
SWART; SW00261; EU; 3.
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SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREDOENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREDUENCY OF 0.2 ALLELE B3 (654-VAL-655) HAS A FREDUENCY OF 0.2 SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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M11761; AAA35808.1

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een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no rest
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); IPR000719; Euk_pkinase.

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01-JAN-1998 (Rel. 06, Created)
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Receptor protein-tyrosine kinase erbB-2
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SMART; SM00261; TYIKC; 1
                         Proto-oncogene;
SIGNAL 1
CHAIN 22
DOMAIN 22
TRANSMEM 655
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Nature 3
[2]
                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An extended family of protein-tyrosine kinase expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                     InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
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Lai C., Lemke G.;
                                                                                                                                                                                                                                                                                                                                                 PIR; A24562; TVRTNU.
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                            EMBL; X03362;
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"The neu_oncogene encodes an epidern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Neuroblastoma;
MEDLINE=86118662; PubMed=3945311;
                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D., "Three dimensional structure of the transmembrane region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPOSINE PHOSPHATE.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECE
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYRO
RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ogenic and oncogenic forms J. 11:43-48(1992). FUNCTION: ESSENTIAL COMPONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
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                                                                                                           PS00107; PROTEIN_KINASE_ATP; 1.
PS00109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
brane; Glycoprotein; Multigene family;
1
22
22
655
678
159
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                                                                                                Tyrosine-protein kinase;
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                                                                                                                                                                                                                Recep_L_domain;
YLP; 2.
                                                                                                                                                                                                                                              pkinase; 1.
Furin-like; 1.
                                                                                 Disease
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                         RECEPTOR PROTE EXTRACELLULAR POTENTIAL.
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CYTOPLASMIC (POTENTIAL)
CYS-RICH.
                                                                     POTENTIAL.
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                                       PROTEIN-TYROSINE
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                                                                                                                                     PYNYLSTEVGSCTLVCPPNNQEVTAEDGTQRCEKCSKPCARVCYGL
                                                                                                                                                                                                 {\tt CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTFGASCVTTC}
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94; Conservative
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85.0%;
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PHOSPHORYLATION (AUTO-) (
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N-LINKED (GLCNAC. )
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BY SIMILARITY.
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PROTEIN KINASE.
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Mismatches
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No. 5.36
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CRC64;
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ERB2_MESAU Q60553; 15-DEC-1998 15-DEC-1998 15-JUN-2002

(Rel. (Rel. (Rel.

37, 37, 41,

Last sequence update)
Last annotation update)

STANDARD;

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DISULFID DISULFID
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ACT_SITE
DISULFID
DISULFID
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Yamazaki Y., Ishikawa T.;
"Cloning and activation of the Syrian hamster neu proto-oncogene.";
Gene 140:251-255(1994).
-i- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE: GP30 IS A
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
ALPHA AND AMPHIREGULIN (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                         PROSITE; PRO0107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.

Transmembrane; Glycoprotein; Multigene family; Receptor; Signal; Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                         Pfam; PF02757; YLP; 2.
ProDom; PD000001; Euk_pkinase;
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINA.
                                                                                                                                                                        Proto-oncogene;
SIGNAL 1
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InterPro; IPR002174; Furin-like
InterPro; IPR001245; Tyr_pkinas;
InterPro; IPR004019; YLP_motif.
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SIMILARITY:
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SUBUNIT: HETERODIMER WITH EACH
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PF00757;
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Furin-like; 1.
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Furin-like.
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                                                                PROTEIN KINASE.

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ATP (BY SIMILARITY).
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                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (E
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VARIANT
             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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 Archosauria; Aves; Neognathae;
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No. 4
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Vertebrata; Euteleostomi;
mes; Phasianidae; Phasianinae;
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MOL. Cell. Biol. 8:1970-1978(1989);
-i- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine-protein SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lax I., Johnson A., Howk R., Sap J., Bellot F., I
Ullrich A., Vennstrom B., Schlessinger J., Givol
"Chicken epidermal growth factor (EGF) receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
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NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor lead dimerization, internalization of the EGF-receptor induction of the tyrosine kinase activity, stimula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + a protein tyrosine
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PF01030; Recep_L_domain; 2.
'; SM00261; FU; 4.
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PS00107; PROTEIN_KINASE_ATP; PARTIAL.

PS00109; PROTEIN_KINASE_TYR; PARTIAL.

PS50011; PROTEIN_KINASE_DOM; PARTIAL.

PS50011; PROTEIN_KINASE_DOM; Signal; Transferase;
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IPR000719; Euk_pkinase.
IPR002174; Furin-like.
IPR001245; Tyr_pkinase.
    AAA48760.1;
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    EGFR_L_domain.
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BY SIMIL
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                                                              Y SIMILARITY
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                                                                                         Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gre Lee J., Yarden Y., Libermann T.A., Schlessinger J., Dc Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H "Human epidermal growth factor receptor cDNA sequence expression of the amplified gene in A431 epidermoid ca. Nature 309:418-425(1984).
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                                                                                                                                                                                                                                                                                                                                                             HUMAN
                     Ilekis J.V., Stark B.C., Scoccia B.; "Possible role of variant RNA transcripts in the epidermal growth factor receptor expression in hu
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=84219729; PubMed=6328312;

Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray

Lee J., Yarden Y., Libermann T.A., Schlessinger J., Down

Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                 Epidermal growth protein-tyrosine
                                                         MEDLINE=95382957; PubMed=7654368
                                                                     TISSUE=Placenta
                                                                                SEQUENCE FROM
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variety of Nature 309: [9]
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                                                                                                                                                                                     Simmen F.A., Gope O'Malley B.W.;
                                                                                                                                                                                              SEQUENCE OF 1028-1210 FROM N.A. MEDLINE-85046483; PubMed-6093780; Simmen F.A., Gope M.L., Schulz T.
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Xu Y.H., Ishii S., Clark A.J.L.,
Roe B.A., Merlino G.T., Pastan I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lampland A.L., Balasubramaniam S., Crossley T Maihle N.J., Human and mouse alternative EGFR transcripts "Human and mouse alternative EGFR transcripts % \left( 1\right) =1
Haley J.D., Wa
          SEQUENCE OF 1-29 FROM N.A. MEDLINE=91107677; PubMed=1988448; Haley J.D., Waterfield M.D.;
                                                                               "The human EGF r
                                                                                                                 SEQUENCE OF 1-29 F
MEDLINE=88217333;
                                                                                                                                                                                                                                           "Human epidermal growth factor receptor cDNA is homologous variety of RNAs overproduced in A431 carcinoma cells."; Nature 309:806-810(1984).
                                                                                                                                                                                                                                                                                                                                                  amplification cells.";
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MEDLINE=84196372; Pt
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Schehl Sinclair C., Pearsall R.S.,
Salasubramaniam S., Crossley T.D.,
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receptor cDNA from
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Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M., Howk R., Givol D., Ullrich A., Schlessinger J.; "All autophosphorylation sites of epidermal growth factor (EGF) receptor and HER2/neu are located in their carboxyl-terminal tails. Identification of a novel site in EGF receptor."; J. Biol. Chem. 264:10667-10671(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the epidermal growth factor receptor ovary fibroblasts.":
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                                                                                                                                                                                                                                                                                                                                                              Carpenter G.
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                                                                                                          family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation. FUNCTION: Isoform 2/truncated isoform may act as an antagonist. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
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l. Acad. Sci. U.S.A. 82:4920-4924(1985).
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EGFR_MOUSE
ID EGFR_MA
AC 001279
OT 91-FEB
DT 15-JUN
DE EPIGER
OS MUS MU
OC EUKARY
OC Mammal
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Best Local :
                   SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSU
MEDLINE=93026370; Pu
Avivi A., Skorecki K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
EMBL;
EMBL;
                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                          Epidermal growth
                                                                                                                                    01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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          Promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed in ovarian cancers.

MISCELLANEOUS: Binding of EGF to the recept dimerization, internalization of the EGF-re induction of the tyrosine kinase activity,
                                                                                                       musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis, and cell proliferation. SIMILARITY: BELONGS TO THE EGF REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X00588;
U95089;
U48722;
U48723;
U48724;
U48724;
U48725;
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                                                                                                                                                                                                                                                    VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR
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                                                                                                                                                                                                                                                                                                                                                                                                            ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                                                                                                                                                                                                                                           KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
 Skorecki K., Yayon A., Givol D.; region of the murine fibroblast growth gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA25240.1; -. AAB53063.1; -. AAC50802.1; -. AAC50804.1; -. AAC50796.1; -. AAC50797.1; -. AAC50798.1; -.
                                        TISSUE-Liver
                                                                                                                                                                              STANDARD;
                                                                                                                           factor
                               PubMed=1408137;
                                                                                   Rodentia;
                                                                                           Chordata;
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45.3%;
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or receptor precursor (E
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Pred. No. 8.4e-54;
                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                              PRT;
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outstation -
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 ProDom; PD000001; Eu SMART; SM00261; FU;
                            Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain
                                                                                                                                                                                                                                                   This
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                                                                                                                                                                                                                      use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hibbs M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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EMBL; X78987; CAA55587.1; -. EMBL; U03425; AAA17899.1; -. EMBL; X59698; CAA42219.1; -. EMBL; L06864; AAA53029.1; -. EMBL; Z12608; CAA78249.1; -. HSSP; P11362; 1FGK.
MGD; MGI:95294; Egfr. InterPro; IPRO00494; Egfr_L_domain. InterPro; IPRO00719; Euk_pkinase. InterPro; IPR002174; Furin-like. InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eisinger D.P., Serrero G.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1992) THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                       entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparison of EGF binding site,";
                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avivi A., Lax I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
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Jenkins N.A., Lee D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94170986; PubMed=8125255;
Luetteke N.C., Phillips H.K., Qiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1994) to the EMBL/GenBank/DDBJ
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MEDLINE=93126380; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91232866; PubMed=2030916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression of the epidermal growth factor recept
in mouse blastocysts during delayed implantation.
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYIL CATTONIC Phosphate.

tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: Binding of EGF to the receptor leads

MISCELLANEOUS: Binding of the EGF-receptor continuation, internalization of the EGF-receptor continuation.
                                                                                                                                                                                                                                                                                                                                                                                                                      synthesis, a
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP + a protein
                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse waved-2 phenotype ptor tyrosine kinase."; s Dev. 8:399-413(1994).
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TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                      and cell proliferation.
: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor sequences
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factor receptor
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Recep_L_domain; Euk_pkinase;

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                                               LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
           YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN------
VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI 184
                    ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                       \verb|LITALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRN|\\
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PS00109;
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                                                                   Conservative
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                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN_KINASE_TYR; 1.
PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                         680
1092
1110
1172
1172
                                                                                                                                                                                                                                          PROTEIN_KINASE_ATP;
                                                                         34.5%;
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175
196
352
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                                                                                                                           N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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C -> S (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Signal; Transier-binding; Phosphorylation;
                                                                         Score 789; DB 1; Pred. No. 1.7e-53;
                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL). APPROXIMATE.
                                                                                                                                                                      N-LINKED
                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                 SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                        APPROXIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

EPIDERMAL GROWTH FACTOR RECEPTOR
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                                                                   Mismatches
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                                                                                                   > S (IN REF. 2).
> W (IN REF. 5).
> F (IN REF. 4).
-> DR (IN REF. 6).
                                                                                              690E20D46DF2D2F5
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                                                                                                                                                              (GLCNAC...)
(GLCNAC...
                                                                                                                                                                                   (GLCNAC. .
                                                                   116;
                                                                                                                                                                                                                    (BY PKC)
(AUTO-) (
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                                                                              Length 1210;
                                                                   Indels
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                                                                                                                                                                                                         MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat
                                                                   22;
                                                                                                                                                                                                         SITE
                                                                 Gaps
                                        73
                                                     89
                                                                  6
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STRAIN-Sprague-Dawley; TISSUE-Sp.....

STRAIN-Sprague-Dawley; TISSUE-Sp.....

RX MEDLINE-97184212; PubMed-9030624;

RX MEDLINE-97184212; PubMed-9030624;

RA Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbett J.A.,

RT "Expression of neuregulins and their putative receptors, ErbB2 and

RT Expression of neuregulins and their putative receptors, ErbB2 and

RT Expression of neuregulins and their putative receptors, ErbB2 and

RT Expression of neuregulins and their putative receptors, ErbB2 and

RT Expression of neuregulins and their putative receptors, ErbB2 and

RT Expression of neuregulins and their putative receptors, ErbB2 and

RT Expression of neuregulins and their putative receptors, ErbB2 and

RT Expression of neuregulins and their putative receptors, RT Expression of neuregulins, NRG-

CC -1- FUNCTION SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-

CC -1- FUNCTION SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-

CC -1- FUNCTION SPECIFICALLY BINDS AND IS ACTIVATED BY NEUREGULINS, NRG-

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CC -1- FUNCTION SPECIFICALLY BINDS AND IS ACTIVATED 
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[2]
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15-DEC-1998 (Rel. 37, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "An extended family of protein-tyrosine kinase expressed in the vertebrate nervous system."; Neuron 6:691-704(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Sciatic ne
MEDLINE=91222560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Neuregulins promote survival and growth of cardiac myocytes Persistence of ErbB2 and ErbB4 expression in neonatal and adventricular myocytes.";
J. Biol. Chem. 273:10261-10269(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98221155; PubMed=9553078;
Zhao Y.-Y., Sawyer D.R., Baliga R
Marchionni M.A., Kelly R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor protein-tyrosine kinase ERBB4 OR TYRO-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 848-901 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERB4_RAT
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                                                                                   RECEPTORS (POTENTIAL).

RECEPTORS (POTENTIAL).

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE DEVELOPING NERVOUS SYSTEM. EXHIBITS DISTINCT AND HIGHLY REGIONALIZED PATTERNS OF EXPRESSION IN THE ADULT BRAIN, WHERE IT IS MAINLY FOUND IN THE RETICULAR NUCLEUS OF THE THALLAMUS. VERY LOW LEVELS IN KIDNEY, AND
                      PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON RESIDUES (BY SIMILARITY). SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baliga R.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; E
Sciurognathi; Muridae;
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erbB-4 precursor
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                                                                       TYROSINE
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InterPro; IPR001245; Tyr_pki
InterPro; IPR004019; YLP_mot
Pfam; PF00757; Furin-1ike; 1
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domai
Pfam; PF02757; YLP; 2.
PRINTS; PR00109; TYRKINASE.
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DISULFID
                                       CARBOHYD
CARBOHYD
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CARBOHYD
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PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP-binding;
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or send a
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SMART; SM00261; FU; 4.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINAS
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SIGNAL
               CARBOHYD
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U52531; AAC53051.1;
P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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IPR002174;
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  Recep_L_domain; YLP; 2.
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   institutions as long
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YLP_motif.
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Furin-like.
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ATP (BY SIMILARITY
ATP (BY SIMILARITY
BY SIMILARITON (I)
PHOSPHORYLATION (I)
PHO
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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CYTOPLASMIC
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             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                     phorbol ester.";
J. Biol. Chem. 2
                                                                                          Plowman G.D., Culouscou J.-M., Whitney G.S., Gree Foy L., Neubauer M.G., Shoyab M.; "Ligand-specific activation of HER4/p180erbB4, a epidermal growth factor receptor family."; proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
                                                                                                                                                                                                                                                                                                                       ERB4_HUMAN STANDARD; PRT; 1308 AA. Q15303; Q15303; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.1: Q180erbB4) (Tyrosine kinase-type cell surface receptor HER4)
                                                                                                                                                                                                                      TISSUE=Breast carcinoma;
MEDLINE=93189574; PubMed=8383326;
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                           tissue distribution
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 ERBB4 OR HER4
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                                                                                       "A novel juxtamembrane
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         FUNCTION: SPECIFICALLY BINDS AND IS ACTIVATED BY PACTOR, NRG-3, HEPARIN-BINDING EGF-LIKE GROWTH FACTOR, NTAK. INTERACTION WITH THESE FACTORS INDUCES CELL NOT ACTIVATED BY EGF, TGF-A, AND AMPHIREGULIN.
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Catarrhini;
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tyrosine
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CELL DIFFERENCIATION
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SMART; SM00261; FU; 4.
SMART; SM00219; TyrKC; 1.
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InterPro;
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                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene f.
                                                                                                                                                                                                                                                                                                                                                                                                                         MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L07868; AAB59446.1; HSSP; P11362; 1FGK.
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ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESS!
BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND
NONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED
CEREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,
KIDNEY, IN ADDITION TO SKELETAL MUSCLE, PARATHYROID, CEREBELLUM,
PITUITARY SPLEEN, TESTIS AND BREAST. LOWER LEVELS IN THYMUS,
LUNG, SALLVARY GLAND, AND PANCREAS.
LUNG, SALLVARY GLAND, AND PANCREAS.
LUNG, SALLVARY GLAND, AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine
SUBUNIT:
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SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
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PF00757; Furin-like; 1.
PF01030; Recep_L_domain
PF02757; YLP; 2.
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); IPR000719; Euk_pkinase;
); IPR002174; Furin-like;
); IPR001245; Tyr_pkinase;
); IPR004019; VLP_motif.
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HOMODIMER OR
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  PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Y SIMILARITY.
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Mammalia; F
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor
(C-exbB3) (Tyrosine kinase-type cell surface rece
                        SEQUENCE FROM N.A.
                                                                                                 ERBB3 OR HER3.
           MEDLINE=90083234; PubMed=2687875;
                                               NCBI_TaxID=9606;
                                                                                     Homo sapiens (Human)
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Miki T., Popescu
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                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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InterPro; IPR000494; EGER_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000714; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase; 1.
Pfam; PF00059; Pkinase; 1.
Pfam; PF00150; Recep_L_domain; 2.
ProDom; PF001010; Euk_pkinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; FAL
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene far
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SEQUENCE FROM P
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DOMAIN
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EMBL; M34309; AAA35979.1; --.
EMBL; S61953; AAB25935.1; --.
PIR; A36223; A36223.
HSSP; P11362; 1FGK.
                                                 SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "c-erbB3 gene encodes secreted as well as transmembrane receptor tyrosine kinase.";
Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-i- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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"Molecular cloning and expression of an additional factor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90311312; PubMed=210 Plowman G.D., Whitney G.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECRETED (SHORT FORM).

ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

DOMALN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).

DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European
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SUBCELLULAR LOCATION: TYPE
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SUBUNIT: HETERODIMER WITH EACH
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                                                                                                                                                                                                                                                                                                                                   HGNC:3431; ERBB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                              equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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sion in a suk
. Acad. Sci.
                                                              splicing
                                                                         e; Glycoprotein; N
Tyrosine-protein
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Y., Sugimura T.,
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tney G.S., Neubauer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th factor receptor family: evidence subset of human mammary tumors."; ci. U.S.A. 86:9193-9197(1989).
RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3 EXTRACELLULAR (POTENTIAL).
                                                                              kinase;
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                                                                         e family; Receptor; Signal;
ATP-binding; Phosphorylation;
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DQTSCVRACPPDKMEVD-KNGLKMCEPCGGLCPKACEGTGS
             DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR---
                                                                  RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG
                                                                                                 NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT
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                             PQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFV-V
                                            PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST
                                                            NGRSCPPCHEVCKG-RCWGPGSEDCQTLTKTICAPQCNGHCFGPNPNQCCHDECAGGCSG
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                                                                                          NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRD---AEIVVKD
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E1LSGGVYIEKNDKLCHMDTIDMADIVRORDAEIVYKDNGR SC.-> GQFPMYPSGLTPQPAQDWYLLDDDPRLLTLSASSK VPVTLAAV (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
LSP-> G (IN REF. 2).
E-> G (IN REF. 2).
E-> G (IN REF. 2).
                                                                                                                                                                                       49;
                                                                                                                                                                                     Score 735.5;
Pred. No. 2.7e
9; Mismatches
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PROTEIN KINASE.
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             -GTHS
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EMBL; U29339;
EMBL; U52530;
HSSP; P11362;
                        PROSITE;
PROSITE;
PROSITE;
                                                                                                                                     Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain;
PRINTS; PR00109; TYRKINASE.
PTCDOM; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Sprague-Dawley; TISSUE-Sciatic nerve; MEDLINE-97184212; PubMed-9030624; Carroll S.L., Miller M.L., Frohnert P.W., Kim S.S., Corbe "Expression of neuregulins and their putative receptors, ErbB3, is induced during Wallerian degeneration."; J. Neurosci. 17:1642-1659(1997).
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                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                               InterPro; IPRO00494; EGFR_L_domain InterPro; IPRO00719; Euk_pkinase. InterPro; IPR002174; Furin-1lke. InterPro; IPR001245; Tyr_pkinase.
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Gene 165:279-284(1995).
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Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor protein-tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE

SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES

AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF

PHOSPHATIDYLINOSITOL 3-KINASE.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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SUBUNIT: HETERODIMER WITH EACH OF
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                        SM00261; FU; 5.
SM00219; TyrK; 1.
E; PS00107; PROTEIN_KINASE_ATP;
E; PS00109; PROTEIN_KINASE_TYR;
E; PS50011; PROTEIN_KINASE_DOM;
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147; Conserv
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CPHNFV-VDQTFCVRACPPDKMEVD-KHGLKMCEPCGGLCPKACEGTGS
                 CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR---GTHS
                                                ECAGGCSGPQDTDCFACRENDSGACVPRCPEPLVYNKLTFQLEPNPHTKYQYGGVCVAS
                                                               QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA
                                                                                                     GAETYVKNNGANCPPCHEVCKG-RCWGPGPDDCQILTKTICAPQCNGRCFGPNPNQCCHD
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POTENTIAL
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XMRK_XIPMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P11362; IFGK.
HSSP, P11362; IFGK.
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                     PRINTS; PRO0109; TYRKINASE.
PRODOM; PD000001; Euk_pkinase; 1
SMART; SM00261; FU; 5.
SMART; SM00210; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; PROTEIN_KINASE
PROSITE; PS00109; PROTEIN_KINASE
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P13388;
O1-JAN-1990
16-OCT-2001
15-JUN-2002
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the Euro
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                                                                                                                                                                       CHAIN
                                                                                                                                                                                           Tyrosine-protein SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xiphophorus maculatus (Southern platyfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Cypinodontiformes; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90015140; PubMed=2797166; Wittbrodt J., Adam D., Malitschek B., Telling A., Robertson S.M., Schartl M
  ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Novel putative receptor tyrosine kinase inducing Tu locus in Xiphophorus."; Nature 341:415-421(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ween the Swiss Institute. There are no results by non-profit institutions as long as its content is iffied and this statement is not removed. Usage by and for institutions and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPOSIDE PHOSPHATE.
SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: INVOLVED IN PICKENT CELLS MALIGNANT MELANOMAS.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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; s06142; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990 (Rel. 13, Created)
001 (Rel. 40, Last sequence update)
002 (Rel. 41, Last annotation updat
receptor protein-tyrosine kinase p
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                                                                                                                                                                                                                                Glycoprotein;
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                                                                                                                                                                                                            kinase;
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PROTEIN_KINASE_DOM;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                          -binding;
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EGFR_DROME STANDARD: PRT: 1426 AA. P04412; O61601; Q9M2G0; P81868; 13-AUG-1987 (Rel. 05, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Epidermal growth factor receptor precursor (EC 2 (Gurken receptor) (Torpedo protein) (Drosophila EGFR OR TOP OR C-ERBB OR DER OR CG10079.

Mandibulata; Pancrustacea; Hexapoda;

2.7.1.112) (Egfr) a relative of ERBB)

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
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RA Barlow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plaischmann W.,
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RA Liu X., Mattei B., McIntosh T.C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Nelson D.L.,
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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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Lesokhin A.M., Yu S.-Y., Katz J., Baker N.E.;
"Several levels of EGF receptor signaling during photoreceptor
specification in wild-type, Ellipse, and null mutant Drosophila.";
Dev. Biol. 205:129-144(1999).
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Clifford R., Schupbach T.;
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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-i- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS,
WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-RAF-
                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=85137938; Pub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A Drosophila genomic sequence growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: UBIOQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORPEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EXER DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX DISK.
                                                                                                                                                                                                                                                                                                                                AND THORACIC AND ABDOMINAL GANGLIA. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine phosphate.
SUBCELLULAR LOCATION: ISOFORMS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS. CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE OCCYTE. IN THE EMBRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTEMACE OF ANNIOSEROSA AND VENTRAL NEUROSCTODERMAL CELLS, GERM BAND RETRACTION. CELL FARES, AND VENTRAL NEUROSCTODERMAL CELLS, GERM BAND RETRACTION OF SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE PROTEINS. ISOFORM TYPE III IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5137938; PubMed=2983232; S.C., Vincent W.S. III,
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L; AF052754; AAC08536.1; JG; AF052753; AAC08536.1; JG; AF052754; AAC08535.1; JG; AF052752; AAC08555.1; JG; K03054; AAA51462.1; JK03417; AAA51460.1; JK03418; AAA51461.1; JK03418;

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Best Local :
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Interpro; IPR000719; E
Interpro; IPR002174; E
Interpro; IPR001245; I
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BINDING
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Receptor; Phosphorylation;
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                                   PLHNQEVTAEDGTQRCEKCSKPCAR
                                                                        KNFFDEAVSKEECPPMRKYNPTTYVLETNPEGKYAYGATCVKECP
                                                                                                            LHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVC
                                                                                                                                               SCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC
                                                                                                                                                                                                                        YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE
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AF109081;
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AF109082;
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AAD26132.
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AAD26133.1;
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EGFR_L_domain.
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RESULT 13
LT23_CAEEL
This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bristol N2;
MEDLINE=96177760; PubMed=8604137;
Sakai T., Koga M., Ohshima Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE-91080919; PubMed=1979659;
Arolan R.V., Koga M., Mendel J.E., Ohshima Y., Sternberg
The let-23 gene necessary for Caenorhabditis elegans vul
"The let-23 gene necessary for Caenorhabditis elegans vul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Let-23 receptor protein-tyrosine kinase precu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT23_CAEEL P24348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitfield C.W., Benard C., Barnes T., Hekimi S., Kim S.K.; "Basolateral localization of the Caenorhabditis elegans epidermal growth factor receptor in epithelial cells by the PDZ protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aroian R.V., Les G.M., Sternberg P.W.;
"Mutations in the Caenorhabditis elegans let-23
elements important for cell-type specificity and
                                                                                                                                                                                                                                                                                                                                                                                   +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1996)
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the nematode C. elegans.";
J. Mol. Biol. 256:548-555(1996)
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Rhabditidae; Pelode:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                             . Biol. Cell 10:2087-2100(1999).

FUNCTION: Tyrosine kinase receptor required for the induction vulval differentiation. Possible receptor for the inductive si required for vulval development. Activated by lin-3 and acts k way of let-60 RAS. The lin-3/let-23 pair is a simplified versi of the mammalian neuregulin-ERNB network.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                    SIMILARITY:
                                                                                                                                                                                                                                                                            DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                      TISSUE
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                                                                                                                                                                                                                                                                         SPECIFICITY: Vulval precursor cells. PMENTAL STAGE: Expressed during L2 ar
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Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                  AL STAGE: Expressed during L2 and L3 BELONGS TO THE EGF RECEPTOR FAMILY
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF000757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
Pr000m; PD000001; Euk_pkinase; 1.
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SMART; SM00261; FU; 6.
SMART; SM00219; TyrKc; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                       ILPR_BRALA
002466;
01-NOV-1997
                                                                                                                                                                                 MOI. Endocrinol. 10:857-866(1996).
-!- FUNCTION: THIS RECEPTOR BINDS
-!- CATALYTIC ACTIVITY: ATP + a pr
                                                                                                                                                                                                                                        MEDLINE=96408719; PubMed=8813726;
Pashmforoush M., Chan S.J., Steiner D.F.;
"Structure and expression of the insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
VARIANT
                                                                                                                                                                                                                               amphioxus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                           tyrosine phosphate.
SUBUNIT: PROBABLE TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINAS DOMAIN (BY SIMILARITY).
SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDP
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> E (IN SY7).
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RECEPTOR SUBFAMILY.

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CARBOHYD
                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
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ACT_SITE
MOD_RES
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PRINTS;
                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
SIGNAL
                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
                                               62
                                                              64
                                                                              12
                                                                                             9
 ILWKDIF --
                 LF-ENYALVVFEMLD-
                           LFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDT
                                                            YLPTNASLSFLQDIQEVQGYVLIAHNQVRQVP----LQRLR------
                                                                            WAALTLYIGLGLLYPSNGEEYICDSMDIRNR-----VSNLRQL-ENCTVIEGYLQI-
                                                                                            WGLL-----LALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELT
                                                                                                             106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00041; fn3;
PF00069; pkina
                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00261;
SM00219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P06213; 1IRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00757;
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             F01030; Recep_L_domain; PR00014; FNTYPEIII. PR00109; TYRKINASE. PD0000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003961;
IPR003962;
IPR002174;
IPR002011;
IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR0007
                                                                                                                                                                                                                                                                             721
929
950
994
1000
1028
1148
1174
                                                                                                                                           51
97
137
278
483
599
665
666
666
711
732
733
733
885
885
                                                                                                             Conservative
                                             LLIDFAEEQDYSGLAFPNLVEITDYFLLYRVRGLTNLSELFPNLAVIRGTN 112
                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pkinase; 1.
Furin-like; 1.
HKNNQLALTLIDTNRSRAC-HPCSPMCK---
                                                                                                                                                                                                                                                                                                                                                                                                                                       FU; 1.
TyrKc; 1.
                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                  720
1363
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1363
1283
1008
                                                                                                                                                  732
736
743
816
885
898
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28.3%;
                                                                                                                                            154104
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Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euk_pkinase.
FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGFR_L_domain
                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation;
                                                                                                                                            MW.
                                                                                                                                                                N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                    Score
Pred.
                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.

ATP (BY SIMILARITY).
                                                                                                                                                                                                        N-LINKED
                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                          CHAIN (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                CHAIN (POTENTIAL).
                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                             PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                INSULIN-LIKE PEPTIDE RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                        INSULIN-LIKE PEPTIDE RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                   342.5; DB
No. 8e-19;
               MQKIGLYSLQNITRGSVRIEKNPNLCYLDT
                                                                                                                                                 (GLCNAC) (GLCNAC) (GLCNAC)
                                                                                                                                                                              (GLCNAC)
                                                                                                                                                                                                                                                   (GLCNAC
(GLCNAC
                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                         DB 1;
                                                                                                            124;
                                                                                                                                                                                                                                                                                                                                                                                         Signal
                                                                                                                                                                                                                                                                           (AUTO-)
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(POTENTIAL).
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                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                           1363;
                                                                                                            105;
                                                            -IVRGTQ
                                                                                                                                                                                                                                                                                                                                                                         ALPHA
                                                                                                           Gaps
                                                            106
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216
               156
                              166
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RESULT
INSR_DE
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10. Created)

11. OV-1997 (Rel. 10, Created)

11. JUN-2002 (Rel. 35, Last sequence updated)

13. Tasulin-like receptor precursor (EC 2.7...

1 INR OR INR-A OR DIR-A.

Drosophila melanona***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishida Y., Hata M., Nishida M., Pishida Y., Hata M., Nishida M., Pishida P., Hata M., Nishida M., Pishida M., Pis
                                                                                                                                                                                                       "Isolation of a Drosophila genomic sequence homologous to the kinase domain of the human insulin receptor and detection of the phosphorylated Drosophila receptor with an anti-peptide antibody."; Proc. Natl. Acad. Sci. U.S.A. 83:4710-4714(1986).

-i- FUNCTION: THIS RECEPTOR PROBABLY BINDS AN INSULIN RELATED PROTEIN AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY (BY SIMILARITY).

-i- CAPALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95181404; PubMed=7876183;
Ruan Y., Chen C., Cao Y., Garofalo R.S.;
"The Drosophila insulin receptor contains a novel carboxyl-terminal extension likely to play an important role in signal transduction."
J. Biol. Chem. 270:4236-4243(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        embryonic development encodes two receptor isoforms with different signaling potential."; EMBO J. 14:3373-3384(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87100165; Pul
Nishida Y., Hata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DROME
                                                                                                                                                                                                                                                                                                                                                                                                                       Birnbaum M.J., Rosen O.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1297-1595 FROM N.A MEDLINE=86259667; PubMed=30145
                                                                                                                                                                                                                                                                                                                                                                                                                                              Petruzzelli L., Herrera R., Arenas-Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Oregon-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 652-1749 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fernandez R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=95354655; PubMed=7628438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fernandez R., Tabarini D., Azpiazu N., Frasch M., Schlessi
"The Drosophila insulin receptor homolog: a gene essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrus
Eusaryota; Metazoa; Arthropoda; Endopterygota; Diptera
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .NSR_DROME
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                                           TYPOSINE PHOSPHATE.

SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED E BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF BINDING DOMAIN, WHILE THE BETA CHAINS CARRY THE KINASE SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D----TFESMPNPEGRY--TFGASCVTACPYNYLSTDVGS---CTLVCPLHNQEVTAEDG
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                            SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=3014506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=3099787;
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2.7.1.112).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pancrustacea; Hexapoda;
Diptera; Brachycera;
                                                    PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fernandez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ebina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlessinger J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar
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THE LIGAND-
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                                                                                                          DOMAIN.
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                                                    INSULIN
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DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00757; Furin-1ike; 1.

DR Pfam; PF00130; Recep_L_domain; 2.

DR PRINTS; PR00109; TyrKINASE.

DR PrODOm; PD000001; Euk_pkinase; 1.

DR SMART; SM00261; FN3; 1.

DR SMART; SM00261; FN3; 1.

DR SMART; SM00261; FN3; 1.

DR ROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

SR PROSITE; PS50011; PROTEIN_KINASE_DOM; Signal.

TY SIGNAL 1

POTENTIAL.
    FlyBase: FBgn0013984; InR.
InterPro: IPR000494; EGFR.L_domain.
InterPro: IPR0007195 Euk_pkinase.
InterPro: IPR003961; FN_III.
InterPro: IPR003961; FN_III.
InterPro: IPR002174; FWIIn-11kc.
InterPro: IPR002114; Tyr_pkinase!.
InterPro: IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U28136; AAA68953.1; -. EMBL; U18351; AAC47458.1; -. EMBL; M14778; AAA28644.1; -. EMBL; M13568; AAA28645.1; -. PIR; A26378; A26378. HSSP; P06213; 1IRK.
CONFLICT
CONFLICT
CONFLICT
                                                              CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
                                                                                                                            CARBOHYD
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BINDING
ACT_SITE
MOD_RES
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DOMAIN
DOMAIN
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CHAIN
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   N-LINKED (GI
N-LIN
                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILA
ATP (BY SIMILA
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Query Match Length DB	DB	ID .	Description
_	2275	99.5	419	4	Q9UK79	O9uk79 homo sapien
2	1716.5	75.1	1259	6	018735	018735 canis famil
ω	794	34.7	527	13	Q90836	090836 qallus qall
4	789	34.5	643	11	Q9ERV6	Q9erv6 mus musculu
5	789	34.5	655	11	Q9WVF5	09wvf5 mus musculu
6	789	34.5	1210	11	Q9EP98	
7	781.5	34.2	1209	11	Q9QX70	
80	773	33.8	478	11	Q9ESE0	
9	734	32.1	331	4	Q9BUD7	Q9bud7 homo sapien
10	723	31.6	149	δ	Q9BG66	Q9bq66 oryctolagus
11	693	30.3	1165	13	Q9YH40	Q9yh40 xiphophorus
12	662.5	29.0	1328	13	P79754	P79754 fuqu rubrip
13	647	28.3	599	<u>1</u> 3	Q9PSH2	Q9psh2 qallus qall
14	571.5	25.0	1433	υ	Q9ВІН9	09bih9 anopheles q
15	463.5	20.3	1137	13	Q9W6F6	09w6f6 gallus gall
16	404.5	17.7	150	6	Q9BG64	Q9bg64 oryctolagus

45 18	44 191	43 20					38 252.5											27 298			30		22 331	353	363	363		17 402
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Q9bh16 anopheles g	Q9n0k4 sus scrofa	016131 caenorhabdi	Q968y9 caenorhabdi	Q9vfe2 drosophila	2	scophti			_				Q8uw84 paralichthy	Q8t0w6 echinococcu	Q9pvz4 xenopus lae	Q9vd94 drosophila	O93457 scophthalmu	073798 xenopus lae	Q9njv5 biomphalari	0	ω		Q26567 schistosoma	Q9y1x8 ephydatia f			Q9bg65 oryctolagus	Q23821 caenorhabdi

ALIGNMENTS

SSULT 1 OSUR79; PRELIMINARY; PRT; 419 AA. OSUR79; O1-MAX-2000 (TrEMBLrel. 13, Created) O1-MAX-2001 (TrEMBLrel. 16, Last sequence update) O1-MAX-2002 (TrEMBLrel. 21, Last annotation update) HER-2. HOMO Sapiens (Human). EUKARYOta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606; [1] SEQUENCE FROM N.A. MEDLINE-99415951; PubMed-10485918; Meddinan J.P., Clinton G.M.; "The HER-2/neu receptor tyrosine kinase gene encodes a secreted autoinhibitor."; Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999). SEQUENCE FROM N.A. SEQUENCE SEQUENCE SEGREL_domain; 1. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE SEQUENCE SEGREL_domain; 1. SEQUENCE 419 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE 419 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C CRC64; SEQUENCE A19 AA; 45472 MW; FECIBE347E2D030C	Qy Db		SQ	DR	DD F	DR	ָ ק ק	RL	R.A	RP	RL	RT	RT	RA	R A	ממ	2 9	8	8	os!	G E	j [3 5	DT	AC	ID	Q R
	1 MELAALCRWGLLLALLPPGAASTOVCTGTDMKLRLPASPETHLDMLRHLYOGCQVVQGNL 	atch 99.5%; Score 2275; DB 4; Length 419; cal Similarity 99.5%; Pred. No. 3e-200; 417; Conservative 1; Mismatches 1; Indels 0; Gaps	SEQUENCE 419 AA; 45472 MW; FEC1BE347E2D030C	SMART; SM00261; FU; 1.	Pfam; PF00/5/; Furin-like; 1. Pfam; PF01030: Recep L domain:			Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.	Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner		Proc. Natl. Acad. Sci. U.S.A.	autoinhibitor.";	"The HER-2/neu receptor tyrosine kinase gene encodes a					Mammalia; Eutheria; Primates; Catarrhini; Hominidae,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;			Uncertain	Ol-MAR-2001 (TremBirel 16,	01-MAY-2000 (TrEMBLrel, 13,	Q9UK79;	9UK79 PRELIMINARY; PRT; 419	RESULT 1 Q9UK79

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Pfam; PF02757; YLP; 2.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM002519; TyrKc; 1.

PROSITE; PS00018; EF_HAND; UNKNOWN_1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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O1-JAN-1998
O1-JAN-1998
O1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cDNA cloning of erbB-2 from Submitted (OCT-1997) to the EEMBL; AB008451; BAA23127.1; HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; 
Mammalia; Eutheria; Carnivora; 
MCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ErbB-2
                                                                                                                                                                                ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
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                                                                                                    Local
  _
                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                        erPro; IPR002048; EF-hand.
erPro; IPR000494; EGFR_L_dom
erPro; IPR000719; Euk_Pkinas;
erPro; IPR002174; Furin-like
erPro; IPR001245; Tyr_pkinas;
erPro; IPR004019; YLP_motif.
n; PF00757; Furin-like; 1.
n; PF00069; pkinase; 1.
n; PF01030; Recep_L_domain;
n; PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MELAAWCRWGLLLALLPSGAAGTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLPPRPAAVPVPLRMQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSLLPRPAAVPVPLRMQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           familiaris (Dog).

Metazoa; Chordata;
                                                                                                Similarity
                                                                                                                                                               1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (TrEMBLrel.
3 (TrEMBLrel.
2 (TrEMBLrel.
                                                                               Conservative
                                                                                                                                                             Transferase; Tyrosine-protein kinase 259 AA; 137989 MW; E37364D49C4ACD46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Euk_pkinase
Furin-like
Tyr_pkinase.
                                                                                                    75
82
                                                                                                                                                                                                                                                                                                                                                                                                                          YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGFR_L_domain.
                                                                                                . 2%;
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05,
21,
                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 m canine mammary gland.
EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
                                                                             Score 1716.5; DB
Pred. No. 2e-148;
4; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1259
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                                                                           49;
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                                                                                                                   6;
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                                                                                                                                                               CRC64;
                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Canis.
                                                                             7;
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419
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                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q90836 PRELIMINARY;
Q90836; TremBLrel. 01, C
01-NOV-1996 (TremBLrel. 01, L
01-JUN-2002 (TremBLrel. 21, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
PLICKING-92123214; PubMed=1732751;
Flickinger T. W., Maihle N.J., Kung H.-J.
"An alternatively processed mRNA from th
soluble, truncated form of the receptor
soluble, truncated formation.";
                                                                                                                                                                                                                                                                                                                                                                            Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dependent transformation.";
mol. Cell. Biol. 12:883-893(1992).
EMBL; M77637; AAA48759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF/TGF-alpha
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00261; FU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000494; EGFR_L_domain
InterPro; IPR002174; Furin-like.
139
                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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TQ--
                                                                                                                                                                                        AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                   TTPVTGASPGGLRELQLRSLTEILKGGYLIQRNPQLCYQDTILWKDIFHKNNQLALTLID
                                                                                                                                                                                                                                                                                                                                                                                                           PF00757; Furin-11xc,
PF01030; Recep_L_domain;
PF01030; FU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                       PTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNN
                                                                                                                                                                    LLLLLGRVALCSAVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLEITYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTLIDTNRFSACPPCSPACKDAHCWGASSGDCQSLTRTVCAGGCARCKGPQPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELTYLPANASLSFLQDIQEVQGYVLIAHSQVRQIPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                 EHNRDLTFLKTIQEVAGYVLIALNMVDVIPLENLQIIRGNVLYDNSFALAVLSNYH-MNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQP
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                                                                                                                                                                                                                                                        al Similarity
155; Conser
                                                                                                                                                                                                                                                                                                                            1
29
527 ,
                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor precursor
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·GLRELPMKRLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PLTVLD
                                                                                                                                                                                                                                                                                                                                                               28
527
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                                                                                                                                                                                                                                                                         34.78;
                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                   Score 794; DB
Pred. No. 2.7e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
EGF/TGF-ALPHA RECEPTOR
764564ABCC095298 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kung H.-J.;
RNA from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                      DB 13;
2.7e-64;
nes 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ne avian c-erbB
that can block
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  189
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Best Local Sim
Matches 156;
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Q9ERV6;
01-MAR-2001 (TIEMBLIEL 1
01-MAR-2001 (TIEMBLIEL 1
01-JUN-2002 (TIEMBLIEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
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EMBL; AF275364; AAG28046.1; JOINED. EMBL; AF275365; AAG28046.1; JOINED. EMBL; AF275365; AAG28046.1; JOINED. MGD; MGI:95294; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C3H/101, 129/SVJ, AND 129/SVETTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C3H/101, 129/SVJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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JerPro; IPR000345; CytC_heme_bind.

JerPro; IPR000494; EGFR_L_domain.

JerPro; IPR002174; Furin-like.

Jerpo; Furin-like; Impro1030; Recep_L_domain; 2.

RT; SM00261; FU; 4.
                                                                                                                                                                                                                                                                                                                                                      ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                       -YGTNRTGLRELPMRNLQEILIGAVRESNNPILCNMDTIQWRDIVQNVFMSNMSMDL---
                                                                                                                                                                VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI 184
                                                                                                                                                                                                                                  YDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAILSN------
                                                                                                                                                                                                                                                                                                                                LLTALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRN
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Rodentia;
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Sciurognathi; Muridae;
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RX MEDLINE-2108560; PubMed=11217851;
RA KAWAI J., Shinadawa A., Shibatak K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinadawa A., Shibatak K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Raicawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Raicawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Szuuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Hawashio S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Nature 409:685-690(2001).
EMBL; AF124513; AAD44149.1;
EMBL; AF275365; AAG28047.1;
EMBL; AF275364; AAG28047.1;
EMBL; AF275365; AAG28047.1;
EMBL; AF275365; AAG28047.1;
EMBL; AK004944; BAB23688.1;
EMBL; AK004941; BAB23662.1;
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O1-NOV-1999 (TrEMBLrel.:
O1-JUN-2002 (TrEMBLrel.:
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Alternative Transcripts from the Human and McCarboxy-Terminal Truncated Receptors.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
Reiter J.L., Threadgill D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C3H/101, 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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Mammalia; Eutheria;
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MBLrel. 12, Last sequence update)
MBLrel. 21, Last annotation update)
factor receptor (Epidermal growth
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Sciurognathi; Muridae;
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r.O., Magnus
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Matches
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Q9EP98;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Epidermal growth factor r
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SEQUENCE FROM N.A.
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen / Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Yee D., Yee D., Lampland A.L., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., Yee D., 
                                                                                                Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., I
Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland
Balasubramaniam S., Crossley T.O., Magnuson T.R., James
                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-C57BL/6J;
Submitted
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                                                                                                                                                                                                                                                                       mouse
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Mammalia; Eutheria;
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                     isoforms
                                    "Comparative genomic mouse alternative Egf
                                                                               Maihle N.J.;
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Local Similarity
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(JUN-2000)
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16, Last sequence update)
21, Last annotation update)
receptor isoform 1.
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EMBL/GenBank/DDBJ
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                                                       analysis
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RESULT

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ID X/O

ID X/O

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AC Q9

AC Q9

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AC Q9

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Best Local
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EMBL; AF275364; AAG28045.1; JOINED.
EMBL; AF275365; AAG28045.1; JOINED.
EMBL; AF275367; AAG28045.1; -.
HSSP; P11362; IFGK.
MGD; MGI:95294; EGfr.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000349; EGFR_L_domain.
InterPro; IPR000749; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002174; Fyrin-like.
InterPro; IPR002174; Tyr_pkinase.
Pffam; PF00757; Furin-like; 1.
Pfam; PF00769; pkinase; 1.
Pfam; PF001030; Recept_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00261; FU; 5.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; TYJKC; 1.

SMART; SM00219; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500119; PROTEIN_KINASE_TYR; 1.

ATP-binding; Receptor; Transferase.

SECTION TO THE TAIL AT A SABAN MAY. 6 CONOCIONAL TRANSFER TO THE TAIL AT A SABAN MAY.
                                                                                                                                                                                                                                          Q9QX70
Q9QX70;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAY-2002
  SEQUENCE FROM N.A. STRAIN=FISHER; TIS MEDLINE=90258888;
                                                                                                                      Rattus norvegicus (
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                    EGFR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340 : || || || || ::|:|| || :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCCHEQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QSHPSSCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -YGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL---
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0 (TrEMBLrel. 13, Last s
2 (TrEMBLrel. 21, Last a
growth factor receptor.
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                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
TISSUE=LIVER;
88; PubMed=2342466;
                                                                                                                                                                        (Rat).
                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.5%;
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134840 MW; 62CD021C9DE32E18 CRC64;
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                                                                                                                                                                                                                                               Last annotation
                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 789;
Pred. No. 2
                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                 PRT;
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.2e-63;
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                                                                                                                           Euteleostomi
; Murinae; Ra
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                                                                                                                           Rattus
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R InterPro; IPRO001719; Euk_pkinase.

R InterPro; IPRO001719; Furin-like.

R InterPro; IPRO00174; Furin-like.

R InterPro; IPRO01245; Tyr_pkinase.

R Pfam; PF00069; Pkinase; 1.

Pfam; PF00069; Pkinase; 1.

PR PRINTS; PR00109; Recept_Ldomain; 2.

PR PRODom; PD000001; Euk_pkinase; 1.

PR PRODom; PD000001; Euk_pkinase; 1.

PR PRODom; PD000001; Fu; 3.

PR PROSITE; SM00261; FU; 3.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TVR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.
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                                                 Q9ESE0;
Q9ESE0;
01-MAR-2001
01-OCT-2001
01-JUN-2002
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FISHER: TISSUE-LIVER: Guttridge K., Dawson T.L., E Submitted (NOV-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1991) [3]
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 Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petch L.A.,
Earp H.S.;
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                                                                                                                                                                                                       PRNYVVTDHGSCVRACGPDYYEV-EEDGVSKCKKCDGPCRK
                                                                                                                                                                                                                               PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR
                                                                                                                                                                                                                                                                                                            CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                           PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGCTGPRESDCLVCHRFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKC
                                                                                                                                                                                                                                                                                                                                                   {\tt MSMDVQRHLTGCPKCDPSCPNGSCWGRGEENCQKLTKIICAQQCSRRCRGRSPSDCCHNQ}
                                                                                                                                                                                                                                                                                                                                                                                    TLIDTNRS-RACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAALCAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                      -----YGTNKTGLRELPMRNLQEILIGAVRFSNNPILCNMETIQWRDIV-QDVFLSN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAVLSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M37394; AAF14008.1;
P11362; 1FGK.
norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                               001 (TrEMBLrel.
001 (TrEMBLrel.
002 (TrEMBLrel.
1 growth factor
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                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LIVER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE
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                               16, Created)18, Last sequence update)21, Last annotation update)receptor related protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Earp H.S.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 781.5;
Pred. No. 1.1e
14; Mismatches
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                                                                                                                       PRT;
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                                                                                                                       478
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Q9BUD7
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            SMART; SM
SEQUENCE
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Query Match
Best Local :
                             Strausberg R.;
Submitted (FEB-2001) to the EMBL/Gen EMBL; BC002706; AAH02706.1; -.
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
Pfam; PF000757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 1.
                                                                                                                                                                                                                                                                                                 Q9BUD7
Q9BUD7;
Q1-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF187818; AAG17037.2; InterPro; IPR000494; EGFR_L_domain. InterPro; IPR0002174; Furin-11ke. Pfam; PF00757; Furin-11ke; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                  TISSUE-PLACENTA;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                     homolog 3.
                                                                                                                                                                                                                                                                                   Similar to v-erb-b2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of a novel regulator of EGFR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=GASTRO-DUODENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLTALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMYNNCEVVLGNLEITYVQRN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QSHPSSCPKCDPSCPNGSCWGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDLSFLKTIQEVAGYFLIALNTVERIPSEDLQIIRGNALYENTYALAILSN------
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                 SM00261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 AA; 53233 MW;
                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
/-erb-b2 avian erythroblastic leukemia v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                 FU;
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45.7%;
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Rodentia;
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 36489
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 MW;
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                                                                                                                 EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.P.N.;
                                                                                                                                                                                                                   Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF873A8376C519E5
45B8EBEE683FE7E8
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                                                                                                                                                                                                                                                                                                                                                                       331
                                                                                                                                                                                                                                    Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         335
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                                                                                                                   databases
CRC64;
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                                                                                                                                                            Query Match
Best Local S
Matches 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BG66;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Receptor tyrosine kinase ErbB2 (Fragment).
                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                               "ErbB genes and epidermal growth factor- (EGF-) like ligands in peri-implantation rabbit uterus and blastocyst."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF333178; AAK14371.1; -. InterPro; IPR002174; Furin-like. Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                             Klonisch T., Wolf P.,
Tetens F., Fischer B
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Klonisch T., Wolf P., Hombach-Klonisch S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BG66
                                                                                                                                                                                                                                                         Kinase
                                                                                                                                                                                                                                                                    SMART; SM00261; FU;
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 121
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                                                                                                         _
                                                                                                                       NPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTR
TFESMPNPEGRYTFGASCVTTCPYNYLST
                                                                     TVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTD 277
                          TFESMPNPEGRYTFGASCVTACPYNYLST
                                                    TICAGGCARCKGQLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTD
                                                                                                       NPQFCYQDTILWQEFSTRTTSWPSTRINASRARTCPPCSPACQASGCWGESPEDCQSLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQTSCVRACPPDKMEVD-KNGLKMCEPCGGLCPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVM-----LNYNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRD----AEIVVKD
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                                                                                                                                                            al Similarity
121; Conserv
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                                                                                                                                                             Conservative
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                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                             149
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                                                                                                                                                                                                                 16240 MW;
                                                                                                                                                                       31.6%;
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                                                                                                                                                            8
                                                                                                                                                            Score 723; DB Pred. No. 1.8e 8; Mismatches
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Pred. No. 4.7e-59;
                                                                                                                                                                                                                 7CB3792A54FC49BA CRC64;
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149
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                                                                                                                                                            DB 6; 1
L.8e-58;
nes 20;
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RESULT 11

Q9YH40

ID Q9YH4

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.

Pfam; PF01030; Recep_L.domain; 2.

PRINTS; PR00109; TYRKINASE.

ProDom; PR00109; TYRKINASE; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TYKC; 1.

PROSITE; PS00109; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS00143; GRAM_POS_ANCHORING; UNKNOWN_1.

PROSITE; PS00110; PROTEIN_KINASE_ANP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.

PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.

PROSITE; PS500109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS500109; PROTEIN_KINASE_TYR; 1.
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Q9YH40;
01-MAY-1999
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000345; Cytc_heme_bind.
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR002189; Gram_pos_anchor.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ EMBL; U53471; AAD10500.2; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dimitrijevic N., Winkler C., Wellbrock C., Gomez A., I Altschmied J., Schartl M.; "Activation of the Xmrk proto-oncogene of Xiphophorus overexpression and mutational alterations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=RIO PURIFICATION;
MEDLINE=98241172; PubMed=9582016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyprinodontiformes;
NCBI_TaxID=8086;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Receptor tyrosine kinase pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schartl
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174
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                                                                                                                                                                                                                                                                                                                                                                                           1 MELAALCRWGLLLALLPPG-AAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQV
TSNPTMNLIPHAFERQCQKCDPGCVNGSCWAPGPGHCQKFTKLLCAEQCNRRCRGPKPID
                                                                                                                                   VLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHK 175
                                                                                                                                                                                                                                                       VQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALA 115
                                                 NNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTD
                                                                                                                                                                                                                                                                                                                                         LELLEL----LLLLLLSIGRCCSTDPDRKVCQGTSNQMTM---LDNHYLKMKKMYSGCNV
                                                                                                                                                                                                                          VLENLEITYTQENQDLSFLQSIQEVGGYVLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 j; Kinase; Transferase; Tyrosine-protein kinase
1165 AA; 129614 MW; 7F7EE38D8771A74E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                         -DVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693; DB 13;
No. 1.3e-54;
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Best Local :
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P79754;
01-MAY-1997 (TrEMBLrel. 0
01-MAY-1997 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Transferase
SEQUENCE 1328 AA; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00757; Furin-like; 1. Pfam; PF00069; pkinase; 1. Pfam; PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gellner K., Brenner S.;
"Analysis of 148 kb of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF056116; AA(
HSSP; P11362; 1FGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 9:251-258(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99177347; PubMed=10077531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000494; EGFR_L_domain
InterPro; IPR000719; Euk_pkinase.
                                                                                                                      183
                302
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                                                                                                                                                                     LNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALT 182
                                                                                                                                                                                                               WGLLLALLPP--GAASTQ----VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLEL
NYLSTDVGSCTLVCPLHNQEVTAEDGTQR-CEKCSKPCAR::: | || || || || || || ::|
                                                                                                        LIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCA 241
                                                                                                                                                                                                                                                   WRLILMCVASRLRAASSQTQEAVCPGTQNGLSSTGSQENQYNLNKDRYKGCEIIMGNLEI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCKGPLDTDCFACRLFNDSGACVPQCPQTLIYNKQTFQMETNPNAKYQYGSICVSQCPT
                                                                                                                                             ----YPKDG--PSGLNQLGLMNLTETLDGGVQIINNKYLRYGPWVYWRDII-RNNDAPIE
                                                                                                                                                                                               TQIESNWDFSFLKTIREVTGYVLIAMNHFQEIPLGQLRVIRGNSLYERRFALSVFLN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVKECPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPK
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                                                               AGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPY 301
                                                                                             IQFNGERGVCH---KSC
                                                                                                                                                                                                                                                                                                         al Similarity
143; Conserv
                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                  29.0%;
42.1%;
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                                                                                          -GNYCWGPGKDQCQILTKTVCAPQCNDRCFGTSPRDCCHIECA
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03,
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; Pred. No. 9.7e-52;
47; Mismatches 125;
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Last sequence update)
Last annotation update)
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epidermal growth factor receptor (Fragment).

Gallus gallus (Chicken).

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00757; Furin-like; 2. Pfam; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A complete description of the EGF-receptor exon implication in oncogenic activation and domain evoncogene 8:2939-2948(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PSH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00261; FU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000494; EGFR_L_domain
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Callaghan T., Antczak M., Flickinger T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=94020816; PubMed=8414496;
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  337
                           475
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  ۳.
                                                                                           DHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPSDCCHNQCAAGCTGPRESDCLACRKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                 VLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGY
                          PGPFHCFSCRFFSRQKECVKQCNILQGEPREFERDSKCLPCHS-ECLVQNSTAYNTTCSG
                                                                                                                                                        SRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNH
                                                                                                                                                                                                                                                                                                                                                RLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PLTVLDFASNLSSVEENGVRKCKK 174
                                                                                                                                                                                                                                                                                                                                                                          SLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID-------
                                                                                                                                                                                                                                                                                                                                                                                                     VLIALNMVDVIPLENLQIIRGNVLYDNSFALAVLSNYH-MNKTQ------GLRELPMK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLEITYVEHNRDLTFLKTIQEVAGY
                                                                               DATCKDTCPPLVLYNPTTYQMDVNPEGKYSFGATCVRECPHNTADRHVCDPLCSDVGCWG
                                                                                                                                                                                      LRSLKEISDGDIAIMKNKNLCYADTMNWRSLFATQSQKTKIIQNRNKNDCCPKCHPNCTE
                                                                                                                                                                                                                                        PKKLDVFRTVKEISGFLLIQAWPDNATLYAFENLEIIRGRTKQHGQYSLAVVNLKIQSLG
                                                                                                                                                                                                                                                                                           CDGLCSKVCNGIGIGELKGILSINATNIDSFKNCTKINGDVSILPVAFLGDAFTKTLPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.3%; ilarity 27.4%; Conservative 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
CAR---GTHSLLPRPAAV 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66363 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 647; DB 13;
Pred. No. 9.4e-51;
2; Mismatches 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEAB46D293D991BD CRC64;
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                                                   -PLHNQEVTAEDGTQRCEKCSK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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PGPDHCMKCAHFIDGPHCVKACPAGV 559

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; 1.

Pfam; PF01030; Recep_L_domain; 2.

Pfam; PF01030; Recep_L_domain; 2.

PF1NTS; PR00109; TYRKINASE;

PF0Dom; PD000001; Euk_pkinase; 1.

SMART; SM00201; TYFKC; 1.

SMART; SM00219; TYFKC; 1.

SMART; SM00219; TYFKC; 1.

PROSITE; PS00110; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BIH9
Q9BIH9
Q9BIH9;
Q9BIH9;
Q1-UN-2001 (TrEMBLrel. 17, Created)
Q1-UN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative epidermal growth factor receptor (Fragment).

Putative epidermal growth factor malaria mosquito).
                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning, expression and localisation of the Anopheles gambiae epidermal growth factor receptor.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ301655; CAC35008.1;
HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002174; Furin-like.
InterPro; IPR002290; Ser_thr_pkin
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000345; CytC_heme_bind
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SUA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7165;
318
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                                                                                                                                                                                                                                                                                      CTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVL
HNQEVTAEDGTQRCEKCSKPCAR
                                                                                       EVG-CWGEGAHNCQRFSKLNCSPQCSQGRCFGPKPRECCHLFCAGGCTGPTQSDCLACKN
                                                                                                                                                                   QLRSLTEILKGGVLIQRNPQLCYQDTILWKDI-FHKNNQLALTLIDTNRSRACHPCSPMC
                                                                                                                                                                                                                                                                     CIGTNGRMSVPANREYHYKNLRDRYTNCTYVDGNLEITWIQNITDLNFLQHIREVTGYVL
                               FYDDGVCKQECPPMQIYNPTNYFWEPNPDGKYAYGATCVRKCP-EHLLKDNGACVRKCPK
                                                                                                                    KGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLH
                                                                                                                                                ELPALRDILGGSVGFFNNYNLCHMKSINWEEILLAPQTSMQYTFNFSSPERVCPPCHPSC
                                                                                                                                                                                                                                         IAHNQVRQVPLQRLRIVRGTQLF-----EDNYALAVLDNGDPLNNTTPVTGASPGGLREL 140
                                                         FNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPL
                                                                                                                                                                                                             ISLYDLPQVILPRLQIIRGRTTFKLNKWEEAYGLFV--
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                            1433
                                                                                                                                                                                                                                                                                                                                 Conservative
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159585 MW; E3D9D88967724F07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                                               Score 571.5;
Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                 Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                 2.4e-43;
                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                            Length 1433;
                                                                                                                                                                                                                                                                                                                                 31;
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                                                                                                                                                  164
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RESULT 15
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00261; FU; 3.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01030; Recep_L_domain;
Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=HINDBRAIN; MEDLINE=99263203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERBB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor tyrosine kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W6F6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinase; Tyrosine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001368; TNFR_c6.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dixon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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180
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                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                    161 LCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVC
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KACDGIGTGSLV 191
                                                                                                                                                                                                                                         AGGC-ARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTF 279
                                                 R----GTHSLL 346
                                                                                                     QLEHNHNAKYTYGAFCVKKCPHNFV-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICP
                                                                                                                                 ESMPNPEGRYTFGASCYTACPYNYLSTDYGSCTLYCPLHNQEYTAEDGTQRCEKCSKPCA 339
                                                                                                                                                                                                              AEQCDGRCYGPYVSDCCHRECAGGCSGPKDTDCFACMNFNDSGACVTQCPQTFVYNPTTF
                                                                                                                                                                                                                                                                                                                   LCFADTIHWQDIVRNPWASNFTLVPTNGSSGCGRCHKSCTG-RCWGPTENHCQTLTKTVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000719; Euk_pkinase.
IPR002174; Furin-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 463.5; DB 1
Pred. No. 1.4e-33;
4; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
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                                                                                                                                                                                                                                                                                                                                                                                                                            73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1137;
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Search completed: March Job time : 50.2751 secs

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Maximum Match 10
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                                                                                                               seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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2287
1 MELAALCRWGLLLALLPPGA.....VGRGPDPDAHVAVNLSRYEG
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Copyright (c) 1993 - 2003
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131.5	142	142	147.5	184.5	196	203	210.5	241.5	257.5	257.5	257.5	257.5	257.5	264.5	264.5	418	493
5.7	6.2	6.2	6.4	8.1	8.6	8.9	9.2	10.6	11.3	11.3	11.3	11.3	11.3	11.6	11.6	18.3	21.6
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US-08-525-940-23	US-09-077-955-34	US-08-644-271-30	US-08-857-076-106	US-08-857-076-104	US-08-857-076-103	US-08-857-076-12	US-08-857-076-105	US-08-746-559A-5	US-08-864-641B-18	US-08-746-559A-2	US-08-625-819-2	US-08-249-687C-2	US-08-746-559A-4	US-09-457-040B-7	US-08-737-715-2	US-09-630-155-1	US-09-046-783-3
Sequence 23, Appl	Sequence 34, Appl	Sequence 30, Appl			Sequence 103, App		Sequence 105, App	5	Sequence 18, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 3, Appli

ALIGNMENTS

Clinton

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RESULT 1
US-09-630-155-2
; Sequence 2, Application US/09630155
; Patent No. 6414130
; GENERAL INFORMATION:
APPLICANT: Doherty, Joni Kristin and Gail M. C
TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
TOTAL OF SEQUENCES: 9
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                                                                                                                                                                                              us-09-630-155-2
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                  Matches 419;
                                                                                                                                                                                                                                                                                                                              TELEPHONE: 206 628-76:
TELEPAX: 206 628-769
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: WINDOWS95
SOFTWARE: WORD
SOFTWARE: WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/630,155
FILING DATE: 16-Jan-2001
CLASSIFICATION: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: DAVISON BETTY L.
REGISTRATION NUMBER: 47,309
REFERENCE/DOCKET NUMBER: 49321-10
61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                          1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: polypeptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
COMPUTER READABLE FORM:
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                                      MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                                                                                            TYPE:
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Conservative
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Query Match
Best Local Similarity
Matches 362; Conserve
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                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulato;
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                    MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                       650-324-0960
               Conservative
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                                                                                                 GM-CSF-Her-2 fusion protein; Fig.
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              Score 1878; DB 2
Pred. No. 4e-156;
9; Mismatches 4
                                               DB 2;
               45;
                                             Length 782;
               Indels
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                                                                                         TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: I
APPLICANT: F
APPLICANT: W
TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
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                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-0880
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                                             TYPE:
                                                                                                                      TELEPHONE:
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Ruegg, Curtis L.
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Best Local Similarity
Matches 362; Conserv
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                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Immunostimulatory Compositions NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Laus, Reiner
                 ATTORNEY/AGENT INFORMATION:
                                                                PRIOR APPLICATION DATA:
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                                                                              APPLICATION NUMBER: US/09/344,195 FILING DATE: 24-Jun-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                   ZIP:
                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
                             APPLICATION NUMBER: US/09/146,283 FILING DATE: 03-SEPT-1998
                                                                                                                                                                                                                                                      COUNTRY:
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Judge, Linda R.
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Pred. No. 4e-156;
9; Mismatches 45
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US-08-467-083-68
Sequence 66, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
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                                                                                                                      APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE RE
TITLE OF INVENTION: FOR DIAGN
TITLE OF INVENTION: HER-2/NEU
                                                                                        CORRESPONDENCE ADDRESS:
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CITY: S
STATE:
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             COUNTRY:
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                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR-----GTHSLLPRPAAVPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
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                                                                                                                                                                                                                                                                                                                                                                                   IQEFAGCKKIFGSLAFLPESFDGDPASNT---APLQPEQLQVFETLEEITGYLYISAWPD
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98104-7092
                                           Seattle
                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 42,702 REFERENCE/DOCKET NUMBER: 76:
                                                        6300 Columbia
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                                                                           Seed and Berry
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                                                                                                                      IMMUNE REACTIVITY TO HER-2/NEU PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES HER-2/NEU ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                     433
                                                            Center,
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                                                            701 Fifth Avenue
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REFERENCE/DOCKET NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 372386 SEEDAMBERRY
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYDE:
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                                                                                        Sequence 68, Application US/08414417B Patent No. 5801005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
 GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE RE
TITLE OF INVENTION: FOR DIAGN
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILLING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                SLPDLSVFQNLQVIRG
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                                                                                                                                                                                                                                                                   IQEFAGCKKIFGSLAFLPESFDGDPASNT---APLQPEQLQVFETLEEITGYLYISAWPD 417
                                                                                                                                                                                                                                                                                                     LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD 405
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83.0%;
 IMMUNE REACTIVITY FOR DIAGNOSIS AND
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Pred. No. 7.5e-156;
9; Mismatches 45;
TO HER-2/neu PROTEIN
TREATMENT OF MALIGNANCIES
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RESULT 7 US-08-484-438-8

Sequence 8, Application US/08484438 Patent No. 5811098

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Seed and Berry LLP
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 418
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolean ""
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CITY: S
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                               YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR-----GTHSLLPRPAAVPVP
                                                                                                                                                                                        AAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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SLPDLSVFQNLQVIRG
                            --PDAHVAVNLSRYEG 419
                                                                                   LRMOPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD 405
                                                                                                                                                                                                                                  LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                                                                                                                                                                                                                                                                                                        DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                                                                                                                                                                                                                                                                                                                  ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                  YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
                                                                                                                                                                        {\tt AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP}
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                                                     IQEFAGCKKIFGSLAFLPESFDGDPASNT---APLQPEQLQVFETLEEITGYLYISAWPD
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Pred. No. 7.5e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Patent No. 5811098 5780031 GENERAL INFORMATION:

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Best Local :
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APPLICATION NUMBER: 08/323
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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   181
                                                                      121
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STRANDEDNESS: unl
TOPOLOGY: unknown
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Local Similarity 83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/981,165 FILING DATE: 24-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
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                                                                DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
              LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                                                                                                                                                       ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                      ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (212) 790-9090
(212) 869-8864/9741
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US-08-486-348A-68
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Best Local S
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FILING DATE: 07-UN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICANT: Cheeve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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TOPOLOGY:
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                                                                                                                                                                                                    Local Similarity
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83.0%;
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                                                                                                                                                                                Score 1878; DB 2;
Pred. No. 7.5e-156;
Prematches 45;
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COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/625,101

FILING DATE: 01-APR-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C7

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900

TELEPAX: (206) 682-6031

INFORMATION TOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
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US-08-625-101-2
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Best Local Similarity
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                                                                             Matches
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CÔMPOUNDS FOR ELICITING OR ENHANCING IMMUNE TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
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CITY: Seattle
STATE: Washing
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6300 Columbia Center, 701 Fifth Avenue
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                                                                             Conservative
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                                                                           Score 1878; DB 2;
Pred. No. 7.5e-156;
9; Mismatches 45;
                                                                                                              Length 1255;
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                                                US-08-468-545B-68
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Query Match
Best Local Similarity
                                                                                                                                                     SOFTWARE: PatentIn Release #1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/468
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cheever, Marti
APPLICANT: Disis, Mary L.
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                                                               linear
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Score 1878; DB 2; Pred. No. 7.5e-156;
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             Length 1255;
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RESULT 11
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APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosyntheti
TITLE OF INVENTION: Marker
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REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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CITY: F
STATE:
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                                                                           NAME: Pitcher, Edmund REGISTRATION NUMBER: 2
                                                                                                                                                                      CLASSIFICATION: 424
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; LENGTH: 1255 amino ac
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-2
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US-08-466-680B-68
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G
                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                               APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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LENGTH: 1255 amino aci
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                                                                                                                                                                            98104-7092
                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                      6300 Columbia Center,
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83.0%;
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Pred. No. 7.5e-156;
9; Mismatches 45;
                                                                                                                                                                                                                                      701 Fifth Avenue
                                                                                                 Version
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Hudzia
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURREMT APPLICATION DATA: APPLICATION NUMBER: US/08/422,10
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
                                                                                                                                                                                                                                       APPLICANT: Shepard, H. Michael
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206),622-4900
                                                                                                                                                                                                            ADDRESSEE: Genentech,
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STREET: 4
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                                                                                                                         94080
                                                                                                                                                                            South San Francisco
                                                                                                                                                                                                                                                                                                                                                                      Application US/08422108
                                                                                                                                                           California
                                                                                                                                                                                              460 Point San Bruno Blvd
                                                                                                                                           USA
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83.0%;
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Pred. No. 7
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Sequence 1, Application US/08422734 Patent No. 6333169

GENERAL INFORMATION:

APPLICANT: Hudziak, Robert M.
APPLICANT: Shepard, H. Michael
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: CITY: S

460 Point San Bruno Blvd

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RESULT 14
US-08-422-734-1
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Best Local Similarity
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PRIOR APPLICATION DATA: 08/355460
APPLICATION NUMBER: 08/355460
APPLICATION 13-DEC-1994
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TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/048346
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAY-1989
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                                                                    DGDPASNT---APLQPEQLQVFETLEEITEYLYISAWPDSLPDLSVFQNLQVIRG
                                                                                                  DLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD--PDAHVAVNLSRYEG
                                                                                                                                    VTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESF
                                                                                                                                                                     VTAEDGTQRCEKCSKPCAR----GTHSLLPRPAAVPVPLRMQPG--PAHPVLSFLRPSW
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82.2%;
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Pred. No. 1
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COUNTRY:

USA

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Best Local Similarity
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/354
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/355460
FILING DATE: 13-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/048346
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                                                                                                                                                                                                                                               121
361 DGDPASNT----APLQPEQLQVFETLEEITEYLYISAWPDSLPDLSVFQNLQVIRG 412
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                                                                                                                                                                                                                                                                                                                      82 GYYLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/4.
                                                                                                                                                                                                                                                                                                                                                                                  22 STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                                                                          GICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSCTLVCPLHNQE 321
                             DLVSAFYSLPLAPLSPTSVPI------SPVSVGRGPD--PDAHVAVNLSRYEG 419
                                                           VTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESF
                                                                              VTAEDGTQRCEKCSKPCAR-----GTHSLLPRPAAVPVPLRMQPG--PAHPVLSFLRPSW
                                                                                                                                                                                                                                                                                                      GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ 120
                                                                                                                                                                                                                                                                                                                                                                  STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ
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82.28;
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Pred. No. 1e-146;
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RESULT 15 US-08-336-708A-9

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Search completed: March Job time: 26.7169 secs
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Matches 151; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08336708A Patent No. 5521295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Pacifici, Rober
APPLICANT: Thomason, Arlen
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Oleski, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Hybrid Receptor Molecules NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                184 LGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGP
                                                                      304
                                                                                                        308 VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340
                                                                                                                                            244 RESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTD
                                                                                                                                                                                248
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                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                           129 VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZTP: 91320-1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                                                                                                              KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD
                                                                                                                                                                                                                                                                                                                                                                                 ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                      HGSCVRACGADSYEM-EEDGVRKCKKCEGPCRK 335
                                                                                                                                                                                                                                                    SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGP
                                                                                                                                                                                                                                                                                        ---ANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNH 183
                                                                                                                                                                                                                                                                                                                                                                                                                                      LLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNNCEVVLGNLEITYVQRN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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               2003, 12:37:12
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Result
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Maximum Match 10
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19: /cgn2_6/ptodata/2/pubpaa/U
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12: /cgn2_6/ptodata/2/pubpaa/U
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        188354 segs, 42170167 residues
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:/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
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       GenCore version 5.1.3 (c) 1993 - 2003 Compus
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US-09-854-356-3
US-09-854-356-7
US-09-854-356-6
US-09-854-356-6
US-09-930-125-2
US-09-931-115-3
0 US-09-821-883-5
0 US-09-821-883-3
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US-09-821-883-4
US-09-854-356-8
US-09-821-883-2
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Sequence 3, Appli
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Sequence 1, Appli
Sequence 118, App
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128.5	128.5	128.5	128.5	128.5	129.5	130.5	133.5	142	147.5	147.5	184.5	184.5	196	196	203	203	210.5	210.5	257.5	771	773	775	793	987	1587
5.6	5.6	5.6				5.7			6.4	6.4	8.1	8.1		8.6									34.7	43.2	69.4
420	420	420	420	420	830	833	420	1940	381	381	370	370	366	366	1724	1724	383	383	1367	615	478	1308	1210	191	289
9	9	9	9	9	9	9	9	9	10	10	10	10	10	10	10	10	10	10	9	10	10	10	10	9	10
US-09-904-011-109	US-09-907-841-109	US-09-907-824-109	US-09-902-853-109	US-09-905-291A-109	US-09-870-759-140	US-10-226-296-5	US-09-796-753-86	US-10-016-283-34	US-09-844-353A-106	US-09-205-658-106	US-09-844-353A-104	US-09-205-658-104	US-09-844-353A-103	US-09-205-658-103	US-09-844-353A-12	US-09-205-658-12	US-09-844-353A-105	US-09-205-658-105	US-09-870-759-120	US-09-940-101-4	US-09-867-521-2	US-09-940-101-2	US-09-725-433-2	US-09-441-411-9	US-09-821-883-23
109,	Sequence 109, App	`	109,	Sequence 109, App	14(Sequence 5, Appli	Sequence 86, Appl	34, Ap	106,	106,	•	Sequence 104, App	103,		Sequence 12, Appl		Sequence 105, App	Sequence 105, App	120,	Sequence 4, Appli	2,	2,	Sequence 2, Appli	9, Ap	Sequence 23, Appl

ALIGNMENTS

RESULT 1 US-09-921-161-1

GENERAL INFORMATION: APPLICANT: Ralph, P

Peter

Sequence 1, Application US/09921161 Patent No. US20020090662A1

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                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANALYTICAL METHOD
FILE REFERENCE: GEMENT.0664
; CURRENT APPLICATION NUMBER: US/09/921,161
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/225,433
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                               us-09-921-161-1
                                                                                                                                                                                                                                                                                                                                SOFTWAND 1 ; SEQ ID NO 1
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                           Matches 362;
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
              241
                                      181
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                                                                                                                                                                                       AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                      LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                                                                                      DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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83.0%;
                                                                                                                                                                                                                                          Score 1878; DI
Pred. No. 1.6e
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nes 45;
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CURRENT APPLICATION NUMBER: US/9/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 3
LENGTH: 653
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Best Local :
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APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
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                             LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD
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TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 712
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Best Local Similarity
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APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals
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SLPDLSVFQNLQVIRG 433
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Pred. No. 1.8e-130;
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RESULT 4 US-09-854-356-6

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GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/new Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
                                                                            Sequence 2, Application US/09769508
Patent No. US20020155527A1
GENERAL INFORMATION:
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LENGTH: 919
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Best Local
    APPLICANT:
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                                 APPLICANT: STUART, SUSAN G. APPLICANT: MONAHAN, JOHN G. APPLICANT: LANGTON, BEATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/493,480 PRIOR FILING DATE: 2000-01-28 PRIOR APPLICATION NUMBER: US 60/117,976 PRIOR EILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin Ver. 2.1
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MONAHAN, JOHN J.
LANGTON, BEATRICE CLAUDIA
HANCOCK, MIRIAM E.C.
CHAO, LORRINE A.
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PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1255
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Best Local Similarity 83.0
'-has 362; Conservative
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TITLE OF INVENTION: C-ERBS-2 EXTERNAL DOMAIN:
FILE REFERENCE: BEBIO-111-C1
CURRENT APPLICATION NUMBER: US/09/769,508
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 1255
TYPE: DET
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                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09854356 Patent No. US20020177567A1
                                                                                                                                                                    APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: Smithkiine Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810pC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
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ORGANISM: Homo sapiens
                    TYPE: PRT
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Pred. No. 3.
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US-09-930-125-2

; Sequence 2, Application US/09930125

; Publication No. US20020193329A1
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: LOCATION: (990)..(1048)
: OTHER INFORMATION: fragment of the phosphorylation domain,
: OTHER INFORMATION: portion (delta PD)
US-09-854-356-1
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APPLICANT: MCNeill, Patricia D.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FO
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MA
FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930,125
CURRENT APPLICATION NUMBER: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity
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LOCATION: (990)...(1255)
OTHER INFORMATION: phosphorylation domain (PD)
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OTHER INFORMATION: extracellular domain (ECD)
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                                                                                                                                                                                                   Cheever, Martin A.
                                                                                                                                                                                     Foy, Teresa M.
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Pred. No. 3.
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; LENTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-930-125-2
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                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 6
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Matches 362; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09441411 Publication No. US20030008342A1
                                                                                                                                                                                                                                                                                                                   APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN
FILE REFERENCE: 730033.409
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/441,411 CURRENT FILING DATE: 1999-11-16
                                                                                                                                                                                 LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                 Score 1878; DB 9;
Pred. No. 3.5e-130;
9; Mismatches 45;
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Pred. No. 3.5e-130;
9; Mismatches 45;
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 9
LENGTH: 1255
TYPE: PRT
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Best Local Similarity 83.0%;
Matches 362; Conservative
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                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens -09-811-123-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
APPLICANT: MARK Sliwkowski
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENENT.073A2
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-5
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
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CURRENT FILING DATE: 2001-03-16
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Pred. No. 3.5e-130;
9; Mismatches 45;
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LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Erickson, Sharon
APPLICANT: Schwall, Ralph
APPLICANT: King, Kathleen
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Best Local
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TITLE OF INVENTION: Compositions and Methods for Del TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30 CURRENT APPLICATION NUMBER: US/09/821,883 CURRENT ETLING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/193,504 PRIOR FILING DATE: 2000-03-30 NUMBER FILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 479
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GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thoma
                                                       Sequence 3, Application US/09821883 Patent No. US20020061310A1
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APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
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                                                                                                                                            KGFLFDIPFDCWKPVQKGAPPPPAHH
                                                                                                                                                                        -----SPVSVGRGPDPDAH 409
                                                                                                                                                                                                                               RPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-------
                                                                                                                                                                                                                                                           ---NFEKLAAP-TRSPNPVTRPWKHVDAIKEALSLLNDMRALENEKNEDVDIISNEFSIQ 389
                                                                                                                                                                                                                                                                                        PLHNQEVTAEDGTQRCEKCSKP----CARGTHSLL---
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pred. No. 3.7e-111;
5; Mismatches 57; 1
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RESULT 13
US-09-821-883-4
                                     TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: HER500* construct US-09-821-883-3
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09821883 Patent No. US20020061310A1
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Best Local Similarity
Matches 319; Conserv
                 SEQ ID NO 4
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
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LENGTH: 697
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Pred. No. 6.3
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                                                                                                                                                                                                                                         Dendritic
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PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEO ID NOS: 26
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 8
ENCITH: 654
                                                         US-09-854-356-8
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US-09-854-356-8
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                            Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                       APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Gheysen, Dirk
APPLICANT: Corrisa Corporation
APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/new Fusion Proteins
                                                                                                                                                                                                                                    FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
                                                                     OTHER INFORMATION:
                                                                                    FEATURE:
                                                                                              ORGANISM: Rattus sp
                                                                                                             TYPE: PRT
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75.48;
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85.0%;
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Pred. No. 8.1e-111;
8; Mismatches 53;
Score 1608.5; DB 9
Pred. No. 1.1e-110;
5; Mismatches 36;
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                            DB 9;
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; OTHER INFORMATION: fragment of the phosphorylation domain, ; OTHER INFORMATION: portion (delta PD) US-09-854-356-2
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APPLICANT: Cheysen, Dirk
APPLICANT: Coriza Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT TLING DATE: 2001-05-09
PRIOR APPLICATION UMBER: US/09/493,480
PRIOR FILING DATE: 2000-01-28
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                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1256
                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09854356 Patent No. US20020177567A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/117,976 PRIOR FILING DATE: 1999-01-29
                                                                                                                                      NAME/KEY: DOMAIN
ILOCATION: (721)...(998)
OTHER INFORMATION: kinase domain (KD)
NAME/KEY: DOMAIN
ILOCATION: (991)...(1256)
OTHER INFORMATION: phosphorylation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 26
                                                                                                                 NAME/KEY: DOMAIN LOCATION: (991)...
                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (1)..(654)
OTHER INFORMATION: extracellular domain (ECD)
                                                                                                                                                                                                                                               LOCATION: (677)..(1256)
OTHER INFORMATION: intracellular domain
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: rat HER-2/neu
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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70.3%; Score 1608.5;
85.0%; Pred. No. 2.36
ative 15; Mismatches
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                               Length 1256;
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Matches

Local Similarity 85.(les 294; Conservative

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Search completed: March 4, 2003, 12:43:46
Job time: 20.6687 secs

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    AAE09196
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HER2 protein conta
Human p68HER-2 ECD
Human p68HER-2 ECD
Human p68HER-2 ECD
HER-2 C-terminal e
Human p68HER-2 ECD
Human p68HER-2 ECD
                                                                                                                                                                                                                                              Description
                                                                                                                                                       Human p68HER-2 ECD
Human p68HER-2 par
HER2 protein conta
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ALIGNMENTS

bone m	Human	AAM74540	22	61	8.9	7	5
brain exp	Human	\vdash	22	61	8.9	7	4
p68HER-2	Human	AAE09215	22	419	٠	12	ū
p68HER-2	Human	50	22	419		12	2
_	Human	AAE09202	22	419		12	Ξ
p68HER-2	Human	AAE09183	22	419	15.2	12	0
Ø	Trunc	AAY97240	21	420	17.7	14	39
truncated	Human	AAE20348	23	419	17.7	14	8
_	Human	AAE09211	22	419	17.7	14	37
p68HER-2	Human	AAE09210	22	419	17.7	14	8
p68HER-2	Human	AAE09209	22	419	17.7	14	5
p68HER-2	Human	AAE09208	22	419	17.7	14	34
p68HER-2	Human	AAE09207	22	419	17.7	14	ü
p68HER-2	Human	AAE09206	22	419	17.7	14	2
p68HER-2	Human	AAE09205	22	419	17.7	14	ĭ
p68HER-2	Human	AAE09204	22	419	17.7	14	ö
p68HER-2	Human	AAE09203	22	419	17.7	14	29
p68HER-2		AAE09200	22	419	17.7	14	8
p68HER-2		AAE09181	22	419	•	14	27
p68HER-2		AAE09216	22	419		15	6
p68HER-2		AAE09213	22	419	•	15	25
_ p68HE		AAE09212	22	419		15	24
HER2 intr		AAE20347	23	79		17	23
p68HER-2		AAE09182	22	79		17	2
n p68HER-2 EC		AAE09180	22	79		17	21
<pre>2 C-termina</pre>		AAY97239	21	79		17	0
p68HER-2	Human	AAE09192	22	79		36	9
n p68HER-2	Huma	AAE09198	22	79		41	8
p68HER-2	Human	AAE09193	22	79		47	7
p68HER-2	Human	AAE09191	22	79		51	9
p68HER-2	Human	AAE09190	22	79		54	5
p68HER-2	Human	AAE09197	22	79		55	4
p68HER-2 EC	Human	AAE09189	22	79		56	ω
Б68н Е	Human	0919	22	79	72.2	57	2
nan HER2 intron	Human	AAE20350	23	79		66	Ξ

RESULT 1 AAE09196 /note= "p68HER-2 ECDIIIa (AAE09184) Pro with Leu" 16-FEB-2001; 2001WO-US05327 Key Misc-difference HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2; ECDIIIa; variant. 15-NOV-2001 AAE09196; AAE09196 standard; peptide; 79 16-FEB-2000; 2000US-0506079. 23-AUG-2001. WO200161356-A1 Homo sapiens. Human p68HER-2 ECDIIIa variant 11 encoded by HER-2 intron (first entry) Location/Qualifiers /note= "p68HER-2 ECDIIIa (AAE09184) Asp substituted with Asn which is encoded by CAC" AA substituted

(UYOR-) UNIV OREGON HEALTH SCI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify collid tumours. The present sequence is p88HER-2 ECDIIIa variant CC solid tumours. The present sequence is not shown in the specification but is contained from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 contained from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                       Misc-difference
                                                                                                                                                                                                                                                   HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Page -; 61pp; English.
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                                                                                                                   Misc-difference
                                                                                                                                                              Domain
                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                        AAE09185 standard;
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                                            Modified-site
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mes 79; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide, which binds treatment of hard tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRGPDPDAHVAVNLSRYEG
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                                                                                                                                                                                                                                        ECDIIIa;
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                                                                                                                                                                                                                                                                                                partial protein containing ECDIIIa variant sequence
                                           /note= "Most commonly occurring substituted with Leu" 75
                                                                                                                                                                            Location/Qualifiers
             /note= "Asn is N-glycosylated. Most commonly occurring
ECDIIIa (AAE09184) Asp substituted with Asn"
                                                                                                    /note=
                                                                                                                                 /note= "Extracellular domain
                                                                                                                                                /label=
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Pred. No. 2e-
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                                                                                                                                 IIIA of p68HER-2"
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                                                                      ECDIIIa (AAE09184) Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                         ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 partial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2001; 2001WO-US05327.
                                                                                                           Unidentified
                                                                                                                                                                                                                                                                         AAE20349 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200161356-A1
               Misc-difference
                                                                                                                                                               Endothelial growth factor receptor; EGFR; tumour; cytostatic; herstatin;
                                        Modified-site
                                                                                                                                                    HER-2
                                                                                                                                                                                                                     18-JUN-2002
                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                              polypeptide, which binds treatment of hard tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-529934/58.
DB; AAD15854.
                                                                                                                                                                                                                                                                                                                                                          GRGPDPDAHVAVNLSRYEG 79
                                                                                                                                    receptor cell tumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ů
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECDIIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Henner WD,
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                         containing
                                                                                                                                    tyrosine kinase; squamous our; cell growth.
                                                                  Location/Qualifiers 1..2
                                       /note=
75..77
            /note= "Asn is N-glycosylated" 81..82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is human p68\mbox{HER-2} partial protein variant sequence.
"Encoded by GGCTGAGACGGCCCCTTCCCCCACCCACCCCACC
                                                     "Encoded by CCCGA"
                                                                                                                                                                                          extracellular domain (ECDIIIa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans A;
                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the extracellular domain of HER-2 for \dot{\phantom{a}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79;
Pred. No.
                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                    cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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/note=

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RESULT 4
AAE09195
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                                                                                                                                                                                                                                                                                                                                                             DЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for treating a solid tumour characterised by endothelial growth factor receptor (EGFR) expression. The method involves administering an agent that binds to an extracellular domain (ECD) of EGFR. The invention also relates to a naturally occurring inhibitor of HER-2 receptor tyrosine kinase called herstatin. The coexpression of herstatin with publisher causes a striking reduction in cell growth that corresponds with suppression of p185 autophosphorylation. The method or a pharmaceutical composition is useful for treating a solid tumour (selected from squamous cell carcinoma, lung carcinoma, colon carcinoma and g1lal cell tumour) characterised by EGFR expression. The present sequence is HER2 protein containing extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating solid tumor characterized by expression of endothelial growth factor receptor, involves administering recombinant herstatin that binds to extracellular domain of the endothelial growth factor receptor
                 Misc-difference
                                                          Homo sapiens
                                                                                  HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                         Human p68HER-2 ECDIIIa variant 10 encoded by HER-2 intron 8
                                                                                                                                                                        15-NOV-2001 (first entry)
                                                                                                                                                                                                                               AAE09195 standard; peptide; 79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2001; 2001WO-US25502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200214470-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ECDIIIa)
                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                             1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                              w
                                                                                                                                                                                                                                                                                                     GRGPDPDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                             GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-269185/31
DB; AAD32539.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 1; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0638834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTCAGTG"
                Location/Qualifiers 73
/note= "p68HER-2 ECDIIIa (AAE09184) Asp substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 79; DB 23; Pred. No. 2.1e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 5
AAE09199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CP 1985HER-2 but contains ECD I, II of the p1854ER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify concleic acids encoding these are useful to treat, diagnose and identify collid tumours. The present sequence is p68HER-2 ECDIIIa variant CC solid tumours. The present sequence is p68HER-2 ECDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 CC (AARF09164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Misc-difference
                                                Homo sapiens
                                                                                 solid tumour; cance
p68HER-2; ECDIIIa;
                                                                                                    HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                         15-NOV-2001
                                                                                                                                                                                                                                                        AAE09199 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clinton G,
                                                                                                                                                   Human p68HER-2 ECDIIIa variant 15 encoded by HER-2 intron 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAE09184).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYOR-) UNIV OREGON HEALTH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2001; 2001WO-US05327
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                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                67 DAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide, which binds to the extracellular domain of HER-2 for treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                DAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                   PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                     (first entry)
                                                                                 cancer; polymorphism; cytostatic; gene therapy
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with Asn which is encoded by CAC"
                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%; Score 73;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans A;
                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
2e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 6
AAE09188
  FH XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel HER-2 (herstatin-2) antagonist comparticularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10^8. The present invention is based upon the initial discovery of an alternative HER-2 invention is based upon the initial discovery of an alternative HER-2 compared to the alternative transcript is a truncated HER-2 protein designated possible. The which lacks the transmerrane and intracellular domains of p189HER-2 which lacks the transmerrane and intracellular domains of p189HER-2 which lacks the transmerrane and intracellular domains of p189HER-2 which lacks the transmerrane and intracellular domains of p189HER-2 which lacks the transmerrane and intracellular domains of the p185HER-2 and the novel ECDIIIa.

The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the collect acids encoding these are useful to treat, diagnose and identify collect acids encoding these are useful to treat, diagnose and identify collect acids encoding these are useful to treat, diagnose and identify collect acids encoded by polymorphic form of human HER-2 intron 8 collect: The present sequence is not shown in the specification but is collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 collected from HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                         Homo sapiens
                                                                               HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                     Human p68HER-2
                                                                                                                                                                                                               15-NOV-2001
                                                                                                                                                                                                                                                           AAE09188
                                                                                                                                                                                                                                                                                                   AAE09188 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 12; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clinton G, Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYOR-) UNIV OREGON HEALTH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity les 73; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of hard tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide, which binds to the extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                 DAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                           DAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.4%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000us-0506079.
                                                                                                                                                                       ECDIIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "p68HER-2 ECDIIIa (AAE09184) Asp substituted with Asn"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                     variant 3 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evans
                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 22;
; Pred. No. 2e-65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α,
                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Вþ
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                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10~8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC meNAA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated CC p6HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 which lacks the transmembrane and intracellular domains of CC contains ECD , II of the p185HER-2 and the novel ECDIIIa.

CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the cc contains encoding these are useful to tract, diagnose and identify concluded an experience is p6HER-2 ECD. The present sequence is p6HER-2 ECD. The present sequence is not shown in the specification but is contained from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 contains the present sequence is not shown in the specification but is contained by polymorphic form of human HER-2 intron 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 72
                                                 HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion; extracellular domain IIIa; antagonist; intron 8; C-terminal extension; truncated HER-2; p68; dimerization inhibitor; cytostatic.
                                                                                                                                                               04-DEC-2000
                                                                                                                                                                                                                                       AAY97241 standard; Protein; 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 6
                                                                                                                           HER-2 C-terminal extracellular domain
                                                                                                                                                                                                    AAY97241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYOR-) UNIV OREGON HEALTH SCI.
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                                                                                                                                                                                                                                                                                                                                                      61 GRGPDPDAHVAV 72
                                                                                                                                                                                                                                                                                                                                61 GRGPDPDAHVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide, which binds to the extracellular domain of \ensuremath{\mathsf{HER-2}} treatment of hard tumors -
                                                                                                                                                                                                                                                                                                                                                                                                    GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 91.1%; Score Similarity 100.0%; Pred. 72; Conservative 0; Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD15857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page -; 6lpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henner WD,
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "p68HER-2 ECDIIIa (AAE09184) Pro substituted
                                                                                                                                                                                                                                       ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
2e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 79,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Homo sapiens

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RESULT 8
AAE09184
Qy
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                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. The CC extracellular domain of pl85-HER-2 is proteolytically shed from breast CC carcinoma cells in culture and is found in serum of some cancer patients CC and may be a serum marker of metastatic breast cancer. An alternative CC elementified. The retained intron is in-frame and encodes a 79 amino acid condensitied of the retained intron is in-frame and encodes a 79 amino acid cestension designated ECDIIIa (the present sequence), which is inserted at residue 340 of pl85-HER-2. The alternative mRNA predicts a truncated CC HER-2 protein (approximately 68 kDa) that lacks the transmembrane and contracellular domains (see AAY97240), p68HER-2 specifically binds to CC dimerization of pl85-HER-2. The p68HER-2. It could therefore block CC dimerization of pl85-HER-2. The p68HER-2 polypeptide binds to a site on the ECD of HER-2 that is different from the site of binding for CC derceptin (RTM) (a marketed humanized monoclonal antibody that is used CC for the treatment of cancer and binds to the ECD of HER-2). The methods, CC compositions, polypeptides and antibodies are used to treat solid CC tumours such as breast cancer, small cell lung carcinoma, ovarian cancer (and/or colon cancer, especially where over-expression of HER-2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                             Homo sapiens
                                                           p68HER-2; ECDIIIa; intron 8
                                                                          HER-2; herstatin; antagonist; extracellular domain;
solid tumour; cancer; polymorphism; cytostatic; gen
                                                                                                                       Human p68HER-2 ECDIIIa domain encoded by HER-2 intron 8.
                                                                                                                                                                                        AAE09184;
                                                                                                                                                                                                                   AAE09184 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Using polypeptides and antibodies that bind to the extracellular domain of the receptor-like tyrosine kinase HER-2 to treat solid tumors of the breast, lung, ovaries and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doherty
                                                                                                                                                         15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page 42-43; 46pp; English
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                                                                                                                                                                                                                                                                                                                                                                 DAHVAV 72
                                                                                                                                                                                                                                                                                                                                    DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-499287/44.
DB; AAA53783.
                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                              83.5%; Score 66; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9905-0234208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adelman JP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                        ECD; Herceptin;
                                                                          therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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AAE09186
ID AAEC
RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is ECDIIIa domain of human p68HER-2 protein encoded by intron 8 of HER-2 gene.
                                                                                                                                                        solid tumour; cancer; polymorphism; cytostatic; gene
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                         HER-2; herstatin; antagonist; extracellular domain;
solid tumour; cancer; polymorphism; cytostatic; gen
                                                                                                                                                                                                                  Human p68HER-2 ECDIIIa variant 1 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clinton G,
                           WO200161356-A1
                                                                                    Misc-difference
                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                 15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                          AAE09186 standard; peptide; 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Fig 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-2000; 2000US-0506079.
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                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide, which binds treatment of hard tumors
                                                                                                                                                                                                                                                                                                                                                                                   DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                               DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US05327
                                                                                       Location/Qualifiers
                                                        with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which binds to the extracellular domain of HER-2 for
                                                                     note= "p68HER-2 ECDIIIa (AAE09184) Thr substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD15869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.5%;
100.0%;
                                                        Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                       therapy;
                                                                                                                                                                                      Herceptin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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23-AUG-2001.

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RESULT 10
AAE09187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody. Herceptin, at an affinity of at least 10°8. The present convention is based upon the initial discovery of an alternative HER-2 invention is based upon the initial discovery of an alternative HER-2 confidence of the alternative transcript is a truncated HER-2 protein designated confidence which lacks the transmembrane and intracellular domains of the plasher-2 but contains ECD I, II of the plasher-2 and the novel ECDIIIa. Confidence of the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the conclete acids encoding these are useful to treat, diagnose and identify collid tumours. The present sequence is po8HER-2 ECDIIIa variant conclete acids encoding these are useful to treat, diagnose and identify collid tumours. The present sequence is po8HER-2 ECDIIIa variant conclete acids encoding these are useful to treat, diagnose and identify collid tumours. The present sequence is po8HER-2 ECDIIIa variant conclete acids encoded by polymorphic form of human HER-2 intron 8.

CC Note: The present sequence is not shown in the specification but is derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                              Misc-difference
                                                                                                                                Homo sapiens
                                                                                                                                                               HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                  Human p68HER-2
                                                                                                                                                                                                                                                                15-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                    AAE09187
                                                                                                                                                                                                                                                                                                                                  AAE09187 standard; peptide; 79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 11; Page -; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clinton G, Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYOR-) UNIV OREGON HEALTH SCI.
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            WO200161356-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      67 DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide, which binds to the extracellular domain of HER-2 for treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.5%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                ECDIIIa variant 2 encoded by HER-2 intron
                                                                              Location/Qualifiers
                                             /note= "p68HER-2 ECDIIIa (AAE09184) Leu substituted with Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 66; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 79;
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RESULT 11
AAE20350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC particularly a polypoptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but containing ECD I, II of the p185HER-2 and the novel ECDIIIa. CT he ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC nucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 ECIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC Note: The present sequence is not shown in the specification but is constructed from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 of the present sequence is not shown in the specification but is considered in the present sequence is not shown in the specification but is considered the polymorphic form because of the present sequence is not shown in the specification but is considered the present sequence is not shown in the specification but is considered the process of the present sequence is not shown in the specification but is considered the process of the present sequence is not shown in the specification but is considered the process of the present sequence is not shown in the specification but is considered from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 of the present sequence is not shown in the specific process of the present sequence is not shown in the specific process of the present sequence is not shown in the specific process of the present sequence is not shown in the specific process of the present sequence is not shown in the specific process of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                   Human; tumour; endothelial growth factor receptor; EGFR; cytostatic;
herstatin; HER-2 receptor tyrosine kinase; squamous cell carcinoma;
colon; glial cell tumour; cell growth.
                                                                                                                                                                                                                                                                                               Human HER2 intron 8
                                                                                                                                                                                                                                                                                                                                          18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          AAE20350;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE20350 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clinton G,
                                                                  21-FEB-2002
                                                                                                             WO200214470-A2
                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-2001; 2001WO-US05327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 66; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0506079
                                                                                                                                                                                                                                                                                               encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.5%; Score 66;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evans A;
                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  core 66; DB 22;
Pred. No. 2e-58;
Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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14-AUG-2001; 2001WO-US25502

14-AUG-2000; 2000US-0638834.

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RESULT 12
AAE09194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for treating a solid tumour characterised by endothelial growth factor receptor (EGFR) expression. The method involves administering an agent that binds to an extracellular domain (ECD) of EGFR. The invention also relates to a naturally occurring inhibitor of HER-2 receptor tyrosine kinase called herstatin. The coexpression of herstatin with p185HER2 causes a striking reduction in cell growth that corresponds with suppression of p185 autophosphorylation. The method or a pharmaceutical composition is useful for treating a solid tumour (selected from squamous cell carcinoma, lung carcinoma, colon carcinoma and glial cell tumour) characterised by EGFR expression. The present sequence is a protein encoded by human HER2 intron 8.
                         16-FEB-2000; 2000US-0506079
                                                                                                          WO200161356-A1
                                                                                                                                                               Misc-difference
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                             HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                               15-NOV-2001
(UYOR-) UNIV OREGON HEALTH SCI
                                                   16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                    Human p68HER-2
                                                                                                                                                                                                                                                                                                                                          AAE09194;
                                                                                                                                                                                                                                                                                                                                                                  AAE09194 standard; peptide; 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating solid tumor characterized by expression of endothelial growth factor receptor, involves administering recombinant herstatin that binds to extracellular domain of the endothelial growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-269185/31.
N-PSDB; AAD32540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; Fig 8; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                       67 DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                  ECDIIIa variant 9 encoded by HER-2 intron 8.
                                                                                                                                 /note= "p68HER-2 ECDIIIa (AAE09184) Pro substituted with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23;
2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 13
AAE09189
망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10-8. The present CC invention is based upon the initial discovery of an alternative HER-2 (CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC molecular contains ECD I. II of the p185HER-2 and the novel ECDIIIa CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC nucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 ECDIII variant CC encoded by polymorphic form of human HER-2 intron 8. CC derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8. (AAE00184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 57
            Clinton G,
                                                                   16-FEB-2000;
                                                                                             16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                      p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                  HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                           Human p68HER-2 ECDIIIa variant 4 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE09189 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clinton G,
                                        (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                          23-AUG-2001
                                                                                                                                                        WO200161356-A1
                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide, which binds to the extracellular domain of HER-2 the treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AAE09184).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
            Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henner WD,
                                                                   2000US-0506079.
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                   /note= "p68HER-2 ECDIIIa (AAE09184) Leu substituted with {\tt Gln}"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.2%;
            Evans A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB; Pred. No. 2.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; 1
. 2.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 14
AAE09197
ID AAE09
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated possessing the strength of the control of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human p68HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is p68HER-2 ECDIIIa variant encoded by polymorphic form of human HER-2 intron 8.

Note: The present sequence is not shown in the specification but is derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8
                        N-PSDB; AAD15866
                                                                                                 Clinton G,
                                                                                                                                                                                                       16-FEB-2000;
                                                                                                                                                                                                                                                       16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                                           23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                              WO200161356-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE09197 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-529934/58
N-PSDB; AAD15858.
                                                WPI; 2001-529934/58
                                                                                                                                                    (UYOR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page -; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 RMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDPDAHVAV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide, which binds to the extracellular domain of HER-2 for treatment of hard tumors \mbox{\ \ -\ }
                                                                                                                                                    UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECDIIIa; variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                 Henner WD,
                                                                                                                                                                                                       2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECDIIIa variant 13 encoded by HER-2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "p68HER-2 ECDIIIa (AAE09184) Arg substituted
with Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.9%;
                                                                                                 Evans A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 22; Pred. No. 2.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 15
AAE09190
ID AAE09
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10.8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-contains polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the CC uncleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 ECDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC Note: The present sequence is not shown in the specification but is contained.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                   Misc-difference
             New polypeptide, which binds to the extracellular domain the treatment of hard tumors -  \\
                                                                N-PSDB; AAD15859
                                                                               WPI; 2001-529934/58
                                                                                                              Clinton G,
                                                                                                                                                                                                                 16-FEB-2001;
                                                                                                                                                                                                                                                    23-AUG-2001
                                                                                                                                                                                                                                                                                     WO200161356-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human p68HER-2 ECDIIIa variant 5 encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE09190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE09190 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-2001 (first entry)
                                                                                                                                               (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                  16-FEB-2000; 2000US-0506079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide, which binds to the extracellular domain of HER-2 for treatment of hard tumors - \,
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                                                                                                              Henner
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                                                                                                                                                                                                                                                                                                                  /note= "p68HER-2 ECDIIIa (AAE09184) Met substituted with Leu which is encoded by ATA" \,
                                                                                                              WD,
                                                                                                                Evans A;
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Search completed: March Job time : 10.1526 secs
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                                                                                                                                                                                                                                                                                                                                     The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is p68HER-2 ECDIIIa variant CC encoded by polymorphic form of human HER-2 intron 8.

CC derived from HER-2 intron 8 encoded ECDIIIa sequence given in figure 8 cannotical for the present sequence is not shown in the specification but is contained.
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                   68.4%; Score 54; DB 22; I larity 100.0%; Pred. No. 2.1e-46; Conservative 0; Mismatches 0;
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Query Match Best Local Matches	RESULT 2 A85032 hypothetical prot C;Species: Arabid C;Date: 16-Feb-20 C;Accession: A850 C;Accession: A850 R;anonymous; The Nature 402, 769-7 A;Title: Sequence A;Reference numbe A;Reference numbe A;Accession: A850 A;Status: prelimi A;Molecule type: 1 A;Residues: 1-865 A;Cross reference C;Genetics: A;Gene: AT4902510 A;Map position: 4	Query Match Best Local Matches Qy 47 PLS	hypothetical protein of Species: Aquifex aee C: Species: Aquifex aee C: Date: 08-May-1998 #: C: Accession: C70311 R: Deckert, G.; Warren V: Deckert, G.; Warren V: Deckert, G.; Warren V: Deckert, G.; Warren V: A; Title: The complete A; Reference number: A A; Accession: C70311 A; Status: preliminary A; Molecule type: DNA) A; Residues: 1-520 <aqa 1-520="" <aqa="" a;="" aq_116="" aquife:<="" c;="" cross-references:="" experimental="" gene:="" genetics:="" gi="" residues:="" source="" superfamily:="" th=""><th>RESULT 1</th><th>30 31 32 33 33 33 34 33 36 37 44 44 44 44 44 44 44 44 44 44 44 44 44</th></aqa>	RESULT 1	30 31 32 33 33 33 34 33 36 37 44 44 44 44 44 44 44 44 44 44 44 44 44
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A;Description: The se
A;Reference number: A
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A;Status: translated
A;Molecule type: DNA
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A;Residues: 1-1503 <KAP>
A;Residues: 1-1503 <KAP>
A;Cross-references: EMBL:AC002330; NID:g2262135; PID:g3892053
A;Experimental source: cultivar Columbia
R;Kalicki, J.; Elliott, G.; Cloud, J.
R;Kalicki to the EMBL Data Library, May 1998
submitted to the EMBL Data Library, May 1998
submitted to the sequence of A. thaliana T14P8.
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A; Reference number: S49910
A; Accession: S49910
A; Moleculo
                                                                                                                                                                                                                                                                                                                                                                                                                                                     chloroplast outer envelope protein OEP86 homolog T10P11.19 - Arabidopsis th N;Alternate names: chloroplast import associated protein, GTP-binding; prot C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Feb-2001 C;Accession: T01098; T01299
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A;Residues: 1-372, Egg/, 376-879 <KES>
A;Cross references: GB:L36857; NID:9576508; PIDN:AAA53276.1; PID:9576509
C;Keywords: chloroplast; GTP binding; membrane protein; nucleotide binding; F;245-252/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                  R:Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Ri, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W. submitted to the EMBL Data Library, November 1998
A;Description: Sequence of A. thaliana BAC T10P11 from chromos
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A;Title: A receptor component of the chloroplast protein translocation machinery.
                                                                                                                                                                                                                                                                         A; Status: translated from GB/EMBL/DDBJ
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hypothetical protein 5 - Rhodopseudomonas blastica C;Species: Rhodopseudomonas blastica C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 C;Accession: S04670 R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E. J. Mol. Biol. 179, 185-214, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 C;Accession: AH1848
R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Nakamura, Y; Sugimoto, M.; Takazawa,
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AH1848
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A;Note: T10P11.19; T14P8.24
C;Keywords: chloroplast; GTP binding; membrane protein; nucleotide binding; P-loop F;862-869/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1503 <KAL>
A;Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193301
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                A; Molecule type: DNA
A; Residues: 1-189 < TYB>
                                                                                                                                                                              A; Reference number: A; Accession: S04670
                                                                                                                                                                                              A; Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and A; Reference number: 504666; MUID: 85058188; PMID: 6209404
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A; Residues: 1-121 <KUR>
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A;Experimental source: strain PCC 7120
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8, 205-213, 2001
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                                                                                                                                                               conceptual translation
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Pred. No. 8.3
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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter C; Bron, S; Brouillet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.; Chd A; Ehrlich, S.D; Emmerson, P.T; Entian, K.D.; Errington, J; Fabret, C; Ferrari, E. Nature 390, 249-256, 1997

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hypothetical protein F58A4.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #t/
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F;10-169/Domain: serine acetyltransferase homology <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:M60090; NID:g142386; PIDN:AAA22162.1; PID:g142390 C;Superfamily: Bacillus serine acetyltransferase; serine acetyltransferase C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-269 <EVA>
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A;Experimental source: strain 168
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R; Kunst, F.; Ogasaw
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C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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    #sequence_revision 06-Jan-1995 #text_change 23-Feb-1997
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A; Residues: 1-382 <STO>
                                            A; Map position:
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A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: B88561
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Best Local Similarity
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A; Accession: S40979
                                                                 R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating A;Reference number: A75000; MUID:99059613; PMID:9851916

A;Reference number: A75000; MUID:99059613; PMID:9851916
                                                                                                                                                                      C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: B88561
                                                                                                                                                                                                                   protein F58A4.7b [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
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B88561
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A; Residues: 1-328 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: G84826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: G84826
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A; Residues: 1-292 <BER>
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RESULT 14
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A97577
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A;Accession: A97577
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Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AH2797
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A; Residues: 1-389 <KUR>
A; Cross-references: GB:
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Science 294, 2323-2328, 2001
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A; Residues: 1-389 <KUR>
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b; Pred. No. 24;
0; Mismatches
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kelz, B.
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C;Date: 15-Sep-2000 **Sequence_
C;Accession: C83470
C;Accession: C83470
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, F
. Lory, S.; Olson, M.V.
                                                                                                                                                                                                              A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                           A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70473
                                                                                                                                                                                                                                                                                                                                                                                                       protoporphyrinogen oxidase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: C83470
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Search completed: March Job time: 10.8835 secs
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A; Residues: 1-436 < AQF>
                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                            Nature 392,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B70473
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A; Residues: 1-397 <STO>
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SL56_HUMAN
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YPQP_BACSU
NIFP_AZOCH
YMH7_CAEEL
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6 gallus gall
7 mus musculu
0 drosophila
2 bacillus fi
1 escherichia
6 desulfuroco
8 odontella s
6 streptomyce
2 aquifex aeo
4 schizosacch
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Query Match Best Local Similarity

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MEDLIND-85058188; PubMed-6209404;

Tybulewicz V.L.J., Falk G., Walker J.E.;
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                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes;
                             "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome."; microbiology 142:2005-2016(1996).
                                                                                    STRAIN=168 / Marburg;
MEDLINE=96349105; PubMed=8760912;
                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein SEQUENCE 189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1075;
STRAIN-168;
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7; Conservative
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RESULT 4
NIFP_AZOCH
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P23145;
01-NOV-1991
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01-JUN-1994
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Hypothetical protein; Complete proteome.
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EMBL; Z99115; CAB14085.1; -.
SubtiList; BG11629; ypqP.
InterPro; IPR003869; Polysac_Capp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                    STANDARD;
                                                                              acetyltransferase
                                                                                                   20, Created)
20, Last sequence up
29, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23286 MW; F3EA64945DE249CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                             8.9%;
                   gamma subdivision; Pseudomonadaceae;

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                          Score 7;
Pred. No.
                                                                                (EC
                                                                                                                       update)
                                                                              update)
2.3.1.30)
                                                                                                                                                                                    269
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                                                                                                                                                                                    AΑ
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Best Local S
Matches 7
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P34474;
01-FEB-1994
01-FEB-1995
15-JUN-2002
             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evans D.J., Jones R., Woodley P.R., Wilborn J.R., Robson R.L.;
"Nucleotide sequence and genetic analysis of the Azotobacter chrococcum nifuSvWZM gene cluster, including a new gene (nifp) encodes a serine acetyltransferase.";

J. Bacteriol. 173:5457-5469(1991).

-i- FUNCTION: PROBABLE SERINE ACETYLTRANSFERASE REQUIRED FOR OPTIMIZING THE EXPRESSION OF NITROGENASE ACTIVITY. NIFP MAN REQUIRED TO BOOST RATES OF SYNTHESIS OR INTRACELLULAR CONCENTRATIONS OF CYSTEINE OR METHIONINE.

-i- CAPALYTIC ACTIVITY: Acetyl-Coa + L-serine = Coa + O-acetyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; D43706: D43706.
InterPro; IPRO01451; Hexapep_transf.
Pfam; PF00132; hexapep; 4.
TIGREAMS; TIGR01172; CysE; 1.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical F58A4.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cysteine biosynthesis SEQUENCE 269 AA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M60090; AAA22162.1; -. PIR; D43706; D43706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPRPAAV
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kDa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nematoda;
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100.0%; Prr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
protein F58A4.7 in ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO THE CYSE/LACA/LPXA/NODL
                                                                                                                                                                                                                                                                                                                                                                                                              oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E0BBCC982E66FDBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acyltransferase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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in chromosome III.
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5. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditida; Rhabditoidea
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RESULT 6
CPM1_ONCMY
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Best Local S
Matches 7
                                                                                                                                                                                   STRAIN-Shasta; TISSUE-Liver;

MEDLINE-98248987; PubMed-9587416;

Yang Y.-H., Wang J.-L., Miranda C.L., Buhler D.R.;

"CYP2M1: cloning, sequencing, and expression of a new cytochrome P450

from rainbow trout liver with fatty acid (omega-6)-hydroxylation
                                                                                                                                                                                                                                                                                             Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; El Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh NCBI_TaxID-8022;
hepatic cytochrome P450 isozymes.";
Biochem. Biophys. Res. Commun. 171:537-542(1990).
-:- FUNCTION: HAS (OMEGA-6)-HYDROXYLATION ACTIVITY TOWARD LAURIC
-:- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)O.
-:- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (
                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 2M1 (EC 1.14.14.1) (CYPIIM1) (Lauric acid omega-6-
                                                                                     Miranda C.L., Wang J.L., Henderson M.C. Regiospecificity in the hydroxylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                    CHARACTERIZATION.
MEDLINE=90386619; PubMed=2403346;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q92088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 APLSPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 APLSPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
TRANSCRIPTION FACTORS. STRONGEST, TO TRANSCRIPTION FACTOR AP-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collab
meen the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                               Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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                                                                                                                                                            Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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113
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EE2B52D1EB3EFD33 CRC64;
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on of lauric acid
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                                                                                       by rainbow
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Best Local
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                                                                                                                                                                                                                                "Nucleotide sequence and structural Drosophila melanogaster."; Mol. Gen. Genet. 211:121-128(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                              P09956; Q24596; Q9V3F1;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1990 (Rel. 16, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
            STRAIN-Berkeley;
                                                                           "Self-association of the
                                                                                                                                                     Pirrotta V., Manet E., Hardon E., Bickel S.E., Benson M., "Structure and sequence of the Drosophila zeste gene.";
                                                                                                                                                                            STRAIN=Oregon-R;
MEDLINE=87218538; PubMed=3582372;
                                                                                                                                                                                                                                                                                   Mansukhani A., Gunaratne P.H., Sherwood P.W., Sneath B.J.,
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                       Regulatory protein zeste.

Z OR EG:BACH59J11.3 OR CG7803.

Drosophila melanogaster (Fruit fly)
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Pfam; PF00067; p450; 1.
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MEDLINE-20196006;
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SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F. Agbayani A., An H.-J. Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Ments S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Renington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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                                                                                                                                                                                                                                                                     Chen J.D., Pirrotta V.;
Chen J.D., Pirrotta V.;
"Multimerization of the Drosophila zeste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Oregon-R;
MEDLINE=20196011; PubMed=10731137;
Benos P.V., Gatt M.K., Ashburner M.,
Barrell B.G., Ferraz C., Vidal S., B.
                                                                                                                                                      SEQUENCE OF 56-323 FROM N.A.
STRAIN-ME-K1, ME-K2, ME-L11, ME-L12,
MEDLINE-93360802; PubMed-8355601;
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                                                                                      "Population genetics and phylogenetics of DNA secmultiple loci within the Drosophila melanogaster
                                                                                                                                                                                                                                                      EMBO J.
                                                                                                                                                                                                                                                                                                                                     MEDLINE-93259149;
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                   . Biol. Evol. 10:804-822(1993).
FUNCTION: INVOLVED IN TRANSVECTION PHENOMENA
GENE EXPRESSION), WHERE THE SYNAPTIC PAIRING
                                                                                                                                        Kliman R.M.;
                                                                                                                                                                                                                                                      12:2075-2083(1993).
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                                                                                                                                                                                                                                                                                                                                                 PubMed=8491197;
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WITH WHICH ZESTE INTERACTS
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EMBL; X06743; CAA29918.1; ALT:
EMBL; L13043; AAA29026.1; -.
EMBL; L13044; AAA29027.1; -.
EMBL; L13045; AAA29028.1; -.
EMBL; L13046; AAA29029.1; -.
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EMBL; AE03324; AAF45783.1; -.
EMBL; AE03324; AAF45783.1; -.
EMBL; AL133505; CAB63525.1; -.
EMBL; A26639, A26639, PIR; S01272; S01272.
PIR; S01272; S01272.
PIR; S12569; S12569.
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16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
16-OCT-2001 (Rel. 40, I
             TISSUE-Intestine;

MEDLINE-99262640; PubMed-10329687;

Mang H., Huang W., Fei Y.-J., Xia H., Yang-Feng T.L., Leibach F.H.,

Devoe L.D., Ganapathy V., Prasad P.D.;

"Human placental Na+-dependent multivitamin transporter. Cloning,

"Human placental Na+-dependent multivitamin transporter."
                                                                                                                                                                                                                                                                                     HUMAN
SL56_F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
CONFLICT
functional expression, gene structure, J. Biol. Chem. 274:14875-14883(1999).
                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                        SLC5A6 OR SMVT
                                                                                                                                                                                                  multivitamin transporter).
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16-OCT-2001 (Rel. 40, Last annotation update)
Sodium-dependent multivitamin transporter (Na(+)-dependent
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574 AA;
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                                                                                                                                                                                                                                                                                       STANDARD;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 18;
0; Mismatches
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S -> A (IN REF. 4 AND 5).
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GLY-RICH.
GLN/ALA-RICH (OPA-REPEAT INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROPHOBIC
                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                       PRT;
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                and chromosomal localization.";
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RESULT 9
GCP3_MOUSE
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Best Local S
Matches 7
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P58854;
15-JUN-2002
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PROSITE;
PROSITE;
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                        Gamma-tubulin
                                                                                         15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dependent multivitamin transporter.";
Arch. Biochem. Biophys. 366:95-106(1999)
-!- FUNCTION: TRANSPORTS PANTOTHENATE, E
                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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EMBL; AF069307; AAD31727.1;
EMBL; AF081571; AAD37481.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Intestine; MEDLINE=99268779;
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SUBCELLULAR LOCATION: Integral
SIMILARITY: BELONGS TO THE SOD
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; NA_SOLUT_SYMP_1;
; NA_SOLUT_SYMP_2;
; NA_SOLUT_SYMP_3;
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" unang W., Fei Y.-J.,
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Last annotation update)
component 3 (GCP-3) (Fr
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Pred. No. 19;
0; Mismatches
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Craniata; Vertebrata; E
Sciurognathi; Muridae;
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SODIUM:SOLUTE
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                                                                      (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                 Length 635;
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                   Euteleostomi;
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 Murinae;
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RESULT 10
CAD2_MOUSE
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Best Local :
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P15116; Q64260;
01-APR-1990 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                             gene.
                                                                                                                                                                                                                               Miyatani S., Shimamura K., Hatta M., Matsunaga M., Hatta K., Takeichi M.; Matsunaga Cadherin: role in selective
                                                                                                                                                                                                                                                           MEDLINE=89346748; PubMed=2762814; Miyatani S., Shimamura K., Hatta
                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                CDH2
                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seq
16-OCT-2001 (Rel. 40, Last ann
Neural-cadherin precursor (N-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
STRAIN=C57BL/6; TISSUE=Testis;
MEDLINE=97033837; PubMed=8879495;
Munro S.B., Blaschuk O.W.;
                                                                                                                                                                                                                       Science 245:631-635(1989).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                  Tamura
                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                       DEVELOPMENTAL STAGE
                                                                                                       Miyatani
                                                                                                                   MEDLINE=92409532; PubMed=1528849;
                                                                                                                              STRAIN=C57BL/6;
                                                                                                                                                                       Submitted
                                                                                          Genomic structure
                                                                                                                                            PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 HPVLSFL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 HPVLSFL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Centrosome (By similarity). SIMILARITY: BELONGS TO THE GCP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleation at the centrosome (By similarity) SUBUNIT: Gamma-tubulin complex is composed of GCP3, GCP4, GCP5 and GCP6 (By similarity).
SUBCELLULAR LOCATION: Centrosome (By similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. FUNCTION: Gamma-tubulin complex is necessary for microtublule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                 Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                      S., Copeland N.G.,
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595
677
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F 78348 MW;
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Last annotation update)
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                                                                 U.S.
                                                                                          chromosomal mapping
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                                                                                                      Gilbert
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; 16A85A47357E33C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                               89:8443-8447(1992).
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                                                                                                      Takeichi
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InterPro; IPR000233; Cadherin_C_term.
pfam; pF00028; Cadherin, 5.
pfam; PF01049; Cadherin_C_term; 1.
                                                                                                                                                                                                                                                                                                                                             PIR;
                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuron 20:1153-1163(1998).

-II - FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS
-ITHEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98318235; PubMed=9655503; Tamura K., Shan W.S., Hendrickson W.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hendrickson W.A.; "Structural basis of cell-cell adhesion by cadherins.";
                                                                                                                                                                   SIGNAL
                                                                                                                                                                                       Cell adhesion;
                                                                                                                                                                                                  PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 374:327-337(1995).
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fetal, immature,
 CARBOHYL
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                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                               ; A32759; IJMSCN.
; 1NCG; 10-JUL-95.
; 1NCH; 10-JUL-95.
; 1NCI; 10-JUL-95.
; 1NCI; 10-JUL-95.
; 1NCJ; 18-MAR-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MICE.
SIMILARITY: CONTAINS 5 CADHERIN DOMAINS
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                                                                                                                                                                                                                                                                                         MGI:88355; Cdh2.
                                                                                                                                                                                                                                                                                                                                                                  AB008811;
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                                                                                                                                                                                                                        ; PR00205; CADH
SM00112; CA; 5
                                                                                                                                                                             3D-structure.
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Legrand J.-F., Als-Nielsen
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1260
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273
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                                                                                                                                                                                                                                   CADHERIN
                                                                                                                                                                                                   CADHERIN_1; 3. CADHERIN_2; 5
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                                                                                                                       POTENTIAL
                                                                                                                                 EXTRACELLULAR
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en J., Colman
(GLCNAC.
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(GLCNAC.
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RESULT 11
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 EMBL;
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Gamma-tubulin complex component 3 (GCP-3) (Spindle pole body protein
Spc98 homolog) (hSpc98) (hGCP3) (h104p).
                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                              Tassin A.-M., Celati C., Moudjou M., Bornens M.; "Characterization of the human homologue of the yeast spc98p and association with gamma-tubulin."; J. Cell Biol. 141:689-701(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98234402; PubMed-9566967;
Murphy S.M., Orbani L., Stearns T.;
"The mammalian gamma-tubulin complex contains homologues spindle pole body components spc97p and spc98p.";
J. Cell Biol. 141:663-674(1998).
                                                                                                                                                                                                                                                                    Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 2 AND TISSUE=Eye, and Muscle;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AN MEDLINE=98234404; Pubmed=9566969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFOF TISSUE=Cervical carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCP3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                    SUBCELLULAR LOCATION: Centrosome.
ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown produced by alternative splicing.
TISSUE SPECIFICITY: Ubiquitously expressed.
SIMILARITY: BELONGS TO THE GCP FAMILY.
                                                                                                                                                                                                                              nucleation at the centrosome. SUBUNIT: Gamma-tubulin complex is composed
                                                                                                                                                                                                                                                        FUNCTION: Gamma-tubulin complex is necessary
AF042378;
AJ003061;
AJ003062;
                                                 non-profit institutions as long as its content
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an email to license@isb-sib.ch).
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AAC39727.1; -. CAA05832.1; -. CAA05833.1; -.
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A -> T (IN REF. 2).
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                 EMBL; AB015718; BAA35073.1;
EMBL; AL133081; CAB61400.1;
HSSP; P24941; 1HCL.
Genew; HGNC:11388; STK10.
                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                              "Molecular cloning of the human gene oriented kinase, and comparative chrc
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MEDLINE=99216434; PubMed=10199912;
Kuramochi S., Matsuda Y., Okamoto
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Mammalia; Eutheria;
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7; Conser
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etazoa; Chordata;
theria; Primates;
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MISSING (IN ISOFORM 3).
T -> S (IN REF. 2).
S -> I (IN REF. 2).
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InterPro;

Ser_thr_pkinase.

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PRINTS; PR00109; TYRKINASE;
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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SEQUENCE FROM N.A.
MEDLINE=95024047; PubMed=7937893;
MEDLINE=95024047; J., Ito S.,
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01-NOV-1995
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase;
                                                                     SEQUENCE
                                                                                         CHAIN
                                                                                                                              InterPro; IPR003687; PSII_PsbK. Pfam; PF02533; PsbK; 1. Photosystem II; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiura M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Em
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                                                                                                                                                                                                 EMBL; D17510; BAA04312.1; ALT_INIT.
                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinus thunbergii (Green
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IPR002290; Ser_thr_pkin
IPR001245; Tyr_pkinase.
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
II reaction center protein K precursor (PSII-K).
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  DB 1;
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es; Pinaceae;
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Pinus.
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Best Local
                                              SEQUENCE FROM N.A.
STRAIN=CV. BE10; TISSUE=Tassel;
MEDLINE=94004987; PubMed=8401606;
                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 01-JUL-1993 (Rel. 01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-CV. Johansen:
MEDLINE-20309318; PubMed=10852478;
MEDLINE-20309318; PubMed=10852478;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 12.8 kDa protein in ycf9-trnS intergenic region (ORF111).
Oenothera hooker1 (Hooker's evening primrose).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCX5_OENHO Q9MTN3;
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                                                                                                                                             Spermatophyta; Magnoliophyta; Panicoideae; Andropogoneae; Z. Panicoideae; Andropogoneae; Z. C. TaxID=4577;
                                                                                                                                                                                                                                                                          MFS14
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01-JUL-1993
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Chloroplast; Hypothetical p
SEQUENCE 111 AA; 12814 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence of the Oenothera elata plastid chromosome, representing plastome I of the five distinguishable Eucenothera plastomes.";
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eurosids II; Myrtales;
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Spermatophyta; Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chiu W.-L., Sears B.;
                       Wright S.Y., Suner M.-M., Bell P.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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     Isolation and characterization of male flower cDNAs from
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12814 MW; E5
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rta; Liliopsida; Poales; Poaceae; PACC cl
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eudicots; Rosi
maize.";
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SIGNAL
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SEQUENCE
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-!- TISSUE SPECIFICITY: ENHANCED EXPRESSION IN MALE FLOWERS.

-!- DEVELOPMENTAL STAGE: ASSOCIATED WITH MICROSPOROGENESIS AND DECLINES AS MATURE POLLEN IS PRODUCED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X67323; CAA47737.1; -. PIR; S25104; S25104. MaizeDB; 69183; -.
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126 AA;
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12653 MW; 67F2813AFF8C55E5 CRC64;
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Maximum DB seq length: 2000000000
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79
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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241					121											Match Length DB	
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Q8TW69	Q95PE1	Q9FMC7	Q8UU36	Q8UU38	8MZA8D	Q8WQU2	Q9HD19	081283	Q9LKR1	Q41010	022774	066518	Q945M4	Q9N6W6	Q9UK79	ID	
Q8tw69 methanopyru	Q95pel amblyomma a	Q9fmc7 arabidopsis	Q8uu36 human immun	Q8uu38 human immun	Q8yzw8 anabaena sp	Q8wqu2 plasmodium	Q9hd19 homo sapien	O81283 arabidopsis	Q9lkr1 pisum sativ	Q41010 pisum sativ	**	O66518 aquifex aeo	Q945m4 arabidopsis	Q9n6w6 drosophila	Q9uk79 homo sapien	Description	

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Q9x8b0 streptomyce Q901a3 human immun															drosophila	Q8yst7 anabaena sp	Q8r814 thermoanaer			Q9i3t2 pseudomonas	shope fibr	Q8uef8 agrobacteri	caenorh	Q9ial2 gallus gall	O81138 arabidopsis		014596 homo sapien

ALIGNMENTS

	7 PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDP 66 	Qy Db
0;	Query Match 83.5%; Score 66; DB 4; Length 419; Best Local Similarity 100.0%; Pred. No. 9.1e-59; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps	
	SEQUENCE 419 AA; 45472 MW; FEC1BE347E2D030C CRC64;	ŞŞ
	SMART; SM00261; FU; 1	DR
	Pfam: PF01030: Recep I domain: 1.	ב ב ב
	InterPro; IPR002174;	DR
	InterPro; IPR000494; EGFR_L	DR
	EMBL; AF177761; AAD56009.2;	DR
		RL.
	Dohorty T K Clinton C M Adolman T D Evans A T Connor	D :
		RP
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	autoinhibitor.";	1 2
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	8
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	Homo sapiens (Human).	SO
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	01-JUN-2002 (TrEMBLrel. 21, Last annotation	DT
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Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-JUN-2002 (TrEMBLrel. 21,
AT49Q2510/T10P11_19.
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InterPro; IPR0031092; HLH, basic.
InterPro; IPR003160; Orange.
pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00351; ORANGE; 1.
PROSITE; PS00038; HELIX, LOOP_HELIX; UNKNOWN_1.
SEQUENCE 217 AA; 24082 MW; 39177C58F322B41
                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                    "Arabidopsis cDNA clones.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; AF412063; AAL06516.1; -.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AJ276313; CAB77019.1;
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Bray S.;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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                                                                                                                                                        J.R.;
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8; Conserv
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llarity 100.0%;
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3a0901s04IAP86;
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O22774:
O1-7AN-1998 (TrEMBLrel. 05, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last seque
O1-JUN-2002 (TrEMBLrel. 21, Last annot
Putative chloroplast outer envelope 86
T10P11.19 OR AT4G02510
                            Aapran N., Johnson D., Schutz K., Gnoj L., Hoffman J., Ti de la Bastide M., Granat S., Hameed A., Gottesman T., Has Shohdy N., Parnell L., Dedhia N., Johnson A.F., Lodhi M., Martienssen R., Chen E.Y., Wilson R., McCombie W.R.; "Sequence of A. thaliana BAC TlOP11 from chromosome IV."; Submitted (NOV-1998) to the EMBL/GenBank/DDRT Aaracantee
                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aquifex aeolicus.
Bacteria; Aquificae;
NCBI_TaxID=63363;
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Kaplan N., Johnson D
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
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EMBL; AE000674; AACO6482.1; -

InterPro; IPR001450; 4Fe4S_ferredoxin.

PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome of aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-VF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     066518;
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SEQUENCE
                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 PAAVPVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PAAVPVPL
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520 AA; 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
N. A.
                                                                                                                                                                                                       N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53603 MW;
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100.0%;
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9472 MW; 979D8B86BF2A20F1 CRC64;
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envelope 86-like protein
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b. 8.3;
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                                                                                                                                                                                                                                                                                                                    Tracheophyta
                                                                                                                                  Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huber
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Best Local S
Matches 8
  Query Match
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Q41010: Q41030;
Q41010- Q41030;
01-JAN-1998 (TrEMBLrel. 05, 101-JUN-2002 (TrEMBLrel. 21, 101-JUN-2002) (TrEMBLrel. 21, 101-JUN-2002)
                                                              NP_BIND
                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing pro
Submitted (MAR-2000) to the
EMBL; AC002330; AAC78265.2; -
EMBL; AL161494; CAB80744.1; -
TIGREAMS; TIGR00993; 3a0901s0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matezo A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAPOD.
Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Eukaryota; Wagnoliophyta; eudicotyledons;
                                                                                                                                               Chloroplast; ATP-binding; TRANSIT 1 146
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF MEDILINE-5063938; Pubmed-7973656; Kessler F., Blobel G., Patel H.V., "Identification of two GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQ
STRAIN-CV. MIRANDA; TISSUE-LEAF;
MEDLINE-95099324; PubMed-7801125;
Hirsch S., Muckel E., Heemeyer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU
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Mayer K.F.X.;
                                                                                                                                                                                        TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein IAP86).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to [3]
                                                                                                                                                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 266:1989-1992(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            import machinery.";
science 266:1035-1039(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
                                                                                                                                                                                                       FUNCTION: INVOLVED IN PROTEIN IMPORT INTO CHLOROPLASTS.
SUBCELLULAR LOCATION: CHLOROPLAST OUTER MEMBRANE.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-31 IS THE
L; L31581; CAA83453.1; -.
L; L36857; AAA53276.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAAVPVPL 591
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8; Conserv
                                                                                                                                                                                    TIGR00993; 3a0901s04IAP86;
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                                             879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muckel E., Heemeyer F., von Heijne G., component of the chloroplast protein
                                                                242
373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                          A
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375
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                                          96548
                                                                                                                                                                                                                                                                                                                                                                                                                 AND SEQUENCE OF
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  10.1%;
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                                          MW;
                                                                                                                                           Outer membrane;
CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
protein OEP86 precursor (GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                  ATP (POTENTIAL).

GPS -> EQQ (IN REF. 2).

; 3BC1C4E9743A0280 CRC64;
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                                                                                                      OEP86
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Length 879;
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Matches
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081283;
01-NOV-1998 (TrEMBLrel 0
01-NOV-1998 (TrEMBLrel 0
01-JUN-2002 (TrEMBLrel 2
T14P8 24 protein
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Q9LKR1
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chloroplast protech import component Toc159.
Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
                        Waterston
Submitted
                                                                                                                                                STRAIN=CV. COLUMBIA;
Kalicki J., Elliott G., Cloud
"The sequence of A. thaliana
                                                                                                                                                                                                                                                                         "The
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryospermatophyta; Magnoliophyta; eudiootytedons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1189 PAAVPVPL 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Initial binding of preproteins involving bypassed during protein import into chlorc Plant Physiol. 122:813-822(2000).
EMBL, AF265939, AAF75761.1;
TIGRRAMS; TIGRO0993; 3a0901s04IAP86; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eurosids I; Fabales; Fabaceae;
                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
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                                                                 STRAIN=CV.
                                                                                                                               Submitted
                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                      WashU;
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
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                                                                                     SEQUENCE FROM N.A.
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8; Conser
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                        (MAY-1998)
                                                                 COLUMBIA;
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158676 MW; AA18A7C3DB5746C4 CRC64;
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21,
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                                                                                                                                                                                                                                                        Sequencing Project.";
the EMBL/GenBank/DDBJ
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yta; eudicotyledons; c
ceae; Papilionoideae;
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                                                                                                                             EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation updat
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                        EMBL/GenBank/DDBJ
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edons; core eudicots; Rosid
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Vicieae; Pisu
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Q9HD19; O1-MAR-2001 (TrEMBLrel. 16, Cre-
01-MAR-2001 (TrEMBLrel. 16, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Scotium-dependent multivitamin t
SMVT OR SLC5A6.
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01-MAR-2002
01-MAR-2002
01-MAR-2002
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SEQUENCE
Wang T., Sam-Yellowe T.Y.; "Conservation of the rhoptry protein Rhop-3 among human Plasmodium species and its potential as a malaria vaccin Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY044910; AAL65267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1222
                                                                                                                                                                                                                                                                                                                       dependent multivitamin transporter, hSMVT.";
Biochim. Biophys. Acta 1574:187-192(2002).
EMBL; AF288781; AAG00587.1; -.
EMBL; AF442149; AAL04706.1; -.
EMBL; AF442150; AAL84707.1; -.
NON_TER
                                                              STRAIN=PF452;
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                           Q8WQU2
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                                                                                           NCBI_TaxID=5833;
                                                                                                     Eukaryota; Alveolata;
                                                                                                                Plasmodium
                                                                                                                          Rhop-3
                                                                                                                                                                                                                                                                                                              SEQUENCE
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"Characterization of the 5' regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21952373; PubMed=11955628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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2 (TrEMBLrel.
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nilarity 100.0%;
Conservative
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Primates;
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160818 MW; 04AEDE84C1BED3F6
                                                                                                     Apicomplexa;
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Pred. No
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Pred. No.
                                                                                                                                                                                                                                                                                                             27CDCC338BD55E9D CRC64;
                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transporter
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human heart
                                                                                                     Haemosporida;
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20;
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jion of
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                                                                                                                                                                                                                                                                                                                                                                                   S.A.,
the h
                            human and rodent vaccine candidate
                                                                                                                                                                                                                                                                     Indels
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                               candidate.";
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RESULT 12
Q8UU38
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Q8YZW8
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Best Local S
Matches 7
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                                                                                                                                                Q8UU38;
Q8UU38;
01-MAR-2002
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01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
         EMBL;
                                                          SEQUENCE FROM N.A.
STRAIN=98CMA307;
MEDLINE=21565561;
                                                                                                                                                                                                                                                                                         InterPro; IPR003477; PemK.

Pfam; PF02452; PemK; 1.

Hypothetical protein; Complete SEQUENCE 121 AA; 13266 MW;
                                                                                                                                                                                                                                                                                                                                                                  Watanabe A., Iriguchi M., Ishinato M., Matsuno Kishida Y., Kohara M., Matsumoto M., Takazawa
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P.,
Watanabe A., Iriguchi M., Ishikawa
                         "Naturally Occurring Protease.";
                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                    cyanobacterium Anabaena sp. DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp.
Bacteria; Cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical ALL0337.
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                   AIDS
                                          Schochetman
                                                                                              NCBI_TaxID=11676;
                                                                                                                                Pol protein
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                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of the filamentous cvanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                             Nakazaki N., Shimpo
Yasuda M., Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=103690;
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|||||||
15 PISPVSV
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                  Res.
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         AF380212;
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7; Conserv
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10212; AAL32185.1;
IPR001995; Asppro
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                                          Kaptue L., Zon G., Hackett
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(TrEMBLrel.
(TrEMBLrel.
(Fragment).
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                Retroviruses 17:1555-1561(2001).
                                                            PubMed=11709100;
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el. 20, La
el. 21, La
All0337.
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Aspprotease_rtrv
                                  Sequence
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Last sequence up
Last annotation
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Last annotation updat
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                                 Polymorphisms
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8E01290F333B1B7A CRC64:
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                                                   Soriano
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RESULT
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Best Local S
Matches 7
          OJFMC7;

01-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (TrEMBLrel. 16, Last sequence update

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Hypothetical 20.3 KDa protein.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryoph
Spermatophyta; Magnoliophyta; eudicotyledons; coeurosids II; Brassicales; Brassicaceae; Arabidop, NCBL_TaxID=3702;
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Best Local
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PROSITE;
NON_TER
CHAIN
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PROSITE;
PROSITE;
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01-MAR-2002
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NON_TER
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDS Res. Hum. Retroviruses 17:1555-1561(2001).
EMBL; AF380214; AAL32187.1;
InterPro; IPR001995; Aspprotease_rtrv.
InterPro; IPR001969; Aspprotease_site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luk K.-C., Kaptue L., Zekeng I
Schochetman G., Hackett J. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21565561; PubMed=11709100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pol protein
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                                                                                                                                                                                                                                                                                                                                                     51 TSVPISP 57
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7 TSVPISP 13
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146
146 AA;
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146
146 AA;
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Pred. No.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEASE
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                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F498137384AB00D6 CRC64;
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                                 Arabidopsis
                                                                  Embryophyta;
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Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
Yamada K., Liu S.X., Pham pr.K., Ee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Ak Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Ak Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
Ak Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Trill Length cDNA of gene MUXI1.15/AT5904830 (GI:9758458).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF360335; AAK28632.1; -.
BMBL; AF360335; AAK28632.1; -.
BMBL; AF360370; AAK93747.1; -.
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                                                                                                                                                                                                       Submitted (MAR-1999) to the EMBL; AF133719; AAK49812.1;
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                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                       Jaworski D.C., Barbour A.G.;
                                                                                                                                                                                                                                                                                                                  SEQUENCE
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"Full Length cDNA of
Submitted (MAR-2001)
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DNA Res. 4:401-414(1997).
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US-09-199-637A-11	US-09-088-651-2	US-08-411-706-4	US-09-386-653A-7	US-09-615-192A-273	US-08-565-386-15	US-09-134-001C-4092	PCT-US93-08528-81	US-08-442-108B-21	US-08-319-052-21	US-08-085-122-11	US-08-118-270-81	PCT-US95-06846A-37	PCT-US94-05083C-37	US-08-467-602-37	US-08-470-339-37	US-08-734-664A-37	US-08-735-021-37	
Sequence 11, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 273, App		Sequence 4092, Ap	Sequence 81, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 11, Appl	Sequence 81, Appl	Sequence 37, Appl	Sequence 37, Appl	`	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	

ALIGNMENTS

TYPE: mino acid STRANDEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: HER-2 ECD antagonist SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-630-155-1 Sequence 1, Application: Sequence 1, Application: Patent No. 6414130 Patent No. 6414130 Patent No. 6414130 Patent No. 6414130 GENERAL INFORMATION: GENERAL INFORMATION: HER-2 BINDING ANTAGONISTS NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: DAVIS WRIGHT TREMAINE LLP ADDRESSEE: DAVIS WRIGHT TREMAINE LLP RESULT 1 US-09-630-155-1 Query Match Best Local Similarity Matches 79; Conserv TELEPHONE: 206 628-7621 TELEFAX: 206 628-7699 INFORMATION FOR SEQ ID NO: 1: APPLICATION NUMBER: US/09/630 FILING DATE: 16-Jan-2001 CLASSIFICATION: CUNKNOWN> ATTORNEY/AGENT INFORMATION: NAME: DAVISON, BARRY L. REGISTRATION NUMBER: 47,309 REFERENCE/DOCKET NUMBER: 4932 TELECOMMUNICATION INFORMATION: 1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60 SOFTWARE: WORD CURRENT APPLICATION DATA: COMPUTER READABLE FORM: SEQUENCE CHARACTERISTICS: GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60 CITY: Seattle STATE: Washington COUNTRY: U.S.A. OPERATING SYSTEM: Windows95 MEDIUM TYPE: Floppy disk COMPUTER: PC compatible ZIP: 98101 Conservative 100.0%; 0; Score 79; DB Pred. No. 2.2 0; Mismatches US/09/630,155 49321-10 DB 4; 2.2e-69; Length 79 Indels 0; Gaps

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61 GRGPDPDAHVAVNLSRYEG 79

US-09-630-155-2 ; Sequence 2, Application US/09630155

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GRGPDPDAHVAVNLSRYEG 79

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                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Finkelstein, Ruth R.
APPLICANT: Lynch, Tim
                                                                                                                                                                                                                            Sequence 2, Application US/09300672 Patent No. 6248937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 79;
                 APPLICANT: Goodman, Howard M.
APPLICANT: Wang, Ming-Li
TITLE OF INVENTION: A TRANSCRIPTION FACTOR REGULATING SEED DEVELOPMENT,
TITLE OF INVENTION: QUALITY AND COLD-TOLERANCE
FILE REFERENCE: 480.89(HY)
CURRENT APPLICATION NUMBER: US/09/300,672
CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 206 628-7621
TELEFAX: 206 628-7699
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        341 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: polypeptide SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: polypep:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Doherty, Joni Kristin and Gail M. Clinton TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/630,155 FILING DATE: 16-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Davison, Barry L.
REGISTRATION NUMBER: 47,309
REFERENCE/DOCKET NUMBER: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DAVIS WRIGHT TREMAINE LLP STREET: 1501 Fourth Avenue, 2600 Century Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows95
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Pred. No. 9.8e-69;
Pred. No. 9.8e-69;
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RESULT 5

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Query Match
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                                                         Matches
                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                              TELEFAX: (617) 876-585 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 328
TYPE: PRT
ORGANISM: Arabidopsis
                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969 FILING DATE:
                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
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CTTY: Cambridge
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                                                      Local Similarity hes 7; Conserv
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                            46 APLSPTS 52
                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                  NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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APLSPTS 15
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LaVallie, E
                                                         Conservative
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-- NO: 11:
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100.0%; Pred. No.
                                                                      100.0%;
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                                                                      DB 2;
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5. 29;
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GENERAL INFORMATION:

Sequence 7, Application US/09306595C Patent No. 6284506

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 1091
TYPE: PRT
ORGANISM: Phaffia rhodozyma
US-09-306-595C-7
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Patent No. 5834247
GENERAL INFORMATION:
APPLICANT: COMB, DONALD G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
TITLE OF INVENTION: ISOPRENOID PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 98108210 PRIOR FILING DATE: 1998-05-06 NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC\_DOS/MS\_DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS,
          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             STREET: 32 TOZ
CITY: BEVERLY
STATE: MASSACH
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                                                                                APPLICATION NUMBER: US 01 FILING DATE: 29-DEC-1995
                                                                   CLASSIFICATION:
                                                                                                                                         CLASSIFICATION:
                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                 USA
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XU, MING-QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOUTHWORTH, MAURICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HODGES, ROBERT A.
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                                                                                                                                                                                                                                                                                                                                                                                                                   MODIFIED PROTEINS, METHODS OF THEIR PRODUCTION AND METHODS FOR PURIFICATION OF TARGET PROTEINS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%; Score 7; DB 4; 100.0%; Pred. No. 83;
                                                                                                  US 08/580,555
                                                                                                                                                                      US/08/811,492
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; INFORMATION FOR SEQ ID NO: 1
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-811-492-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
""" 6; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/08036555B Patent No. 5530109
                               CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/965,173

FILING DATE: 23 OCT-1992

PRIOR APPLICATION UMBER: 07/940,389

FILING DATE: 03-SEP-1992

PRIOR APPLICATION UMBER: 07/907,138

APPLICATION NUMBER: 07/907,138

FILING DATE: 30-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/f
APPLICATION NUMBER: US 08/f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555B
FILING DATE: 24 MAR-1993
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
ZIP: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
STATE:
APPLICATION NUMBER: 07/863,703 FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
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                                                                                                                                                                                                                                                                                                                                                                                                    10022
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03-NOV-1993
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Pred. No
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APPLICATION NUMBER:

10-APRIL-1991

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Query Match
Best Local Similarity
Thehes 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Minghetti, Lull APPLICANT: Minghetti, Lull APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles, Lul APPLICANT: Chen, Maio Su; Hiles
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/96
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/94
FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/036,555
APPLICATION NUMBER: 24-MAR-1993
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                       PRIOR APPLICATION DATA:
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NAME: Tsai, Christine H.
                             ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/907,138 FILING DATE: 30-JUN-1992
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SOFTWARE: Wordperfect
REGISTRATION
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                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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minghetti, Luisa; Waterfield, Michael; Marchioni,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 5.25 inch, 360 kb storage
                                                                                                  10-APRIL-1991
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                                                                                                                                      U.K. 91 07566.3
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Pred. No
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Best Local Similarity
"~+~hes 6; Conserv:
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APPLICANT: Goodea:
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                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 26 MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                        APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07:
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-OCT-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
NAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 250.4
TELECOMMUNICATION: TOPORMATION:
                                                                      FILING DATE: 10-APRIL-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/940,389 FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/0 FILING DATE: 24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 SPVSVG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodearl, Andrew; Stroobant, Paul;
Minghetti, Luisa; Waterfield, Michael; Marchioni,
Chen, Maio Su; Hiles, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                    23-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             838-3884
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                                                                                                                                                                                                                                                                                                                                                                       08/036,555
                                                                                                             U.K. 91 07566.3
                                                                                                                                                                                                                07/907,138
                                                                                                                                                                                                                                                                                                                     07/965,173
                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/249,322A
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8; Pred. No. 17;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 06 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036
FILING DATE: 24-MAR-1993
                               TELEFAX: 617-428-7045 NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
                                                            TELEPHONE: 617-428-0200
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HILES, IAN
APPLICANT: HILES, TAN
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 03-APF APPLICATION NUMBER:
                                                                                                                                                                                                                    APPLICATION NUMBER: 07/9 FILING DATE: 03-JUN-1992
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                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/940,389 FILING DATE: 03-SEP-1992
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Minghetti, Luisa
Waterfield, Michael
Marchionni, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                        03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                                                                                                                                                                                                                06 June 1995
                                                                                                                                                            10-APR-1991
                                                                                                                                                                                                                                                                                    23-OCT-1992
                                                                                                                                                                         U.K. 91 07566.3
                                                                                                                                                                                                       07/863,703
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                                                                                             04585/00200A
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Mismatches
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US-08-469-526A-49
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US-08-734-591A-49
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                                           APPLICATION NUMBER: UK 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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PRIOR APPLICATION UNMEER: 08/036,555

FILING DATE: 03-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173

FILING DATE: 23-OCT-1992
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      APPLICATION NUMBER: 07/8
FILING DATE: 03-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect (Version 7.0) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/907,138 FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/470,335 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 22-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible Pentium OPERATING SYSTEM: Windows95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
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Minghetti, Luisa
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 Mismatches

                                                                                     04585/00200P
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Pred. No.
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). 17;
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US-08-734-591A-49

TYPE: amino a STRANDEDNESS: TOPOLOGY: lin

linear

amino acid

SEQUENCE CHARACTERISTICS: LENGTH: 15

Query Match

Length 15;

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                                                                                                TOPOLOGY: US-08-469-660-49
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US-08-469-660-49
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                              Best Local Similarity 100.0%; I Matches 6; Conservative 0;
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,396
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/984,085
FILING DATE: 01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                             TELEFAX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gwynne, Lavie, APPLICANT: McBurney, Robert N.
APPLICANT: McBurney, Robert N.
TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
THEIR PREPARATION AND USE
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/951,747
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                   TELEPHONE: (bi, , 200154
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 56 SPVSVG 61
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 10-AUC
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                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
ZIP: 0211-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                LENGTH:
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                                                                                                                                             amino acid
                                                                                                                 linear
                                                                                                                                                                                                                             (617) 542-5070
                                                                                                                                                                                                                                                                                                                           UMBER: 07/927,337
10-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 6; DB 2;
100.0%; Pred. No. 17;
                                                                7.6%;
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                                                                                                                                                                                                49:
                                                                                                                                                                                                                                                              04585/017004
                              Score 6; DB;; Pred. No. 17; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                              DB 2;
                              0;
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                            Gaps
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                              0;
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; SEQ ID NO 82
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-341-018-82
 В
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                                                Query Match
Best Local Similarity
Trackes 6; Conserve
                                                                                                                                 ; ORGANISM: Bos taurus US-08-470-335-49
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Best Local Similarity
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; Sequence 82, Application US/08341018A 
; Patent No. 6087323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                  SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 49
LENCTH: 15
TYPE: PRT
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                                                                                                                                                                                                                                FILE REFERENCE: 04585/00200B
CURRENT APPLICATION NUMBER: US/08/470,335F
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
EARLIER FILING DATE: 1993-03-24
NUMBER OF SEQ ID NOS: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MCBUTNCY, ROBET N.
TITLE OF INVENTION: USE OF NEUERGULINS AS MODULATORS
TITLE OF INVENTION: CELLULAR COMMUNICATION
FILE REFERENCE: 04585/041001
CURRENT APPLICATION NUMBER: US/08/341,018A
CURRENT FILING DATE: 1394-11-17
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: STROOBANT, PAUL
APPLICANT: MINGHETTI, LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: WARCHIONNI, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gywnne, David I.
APPLICANT: Mahanthappa, Nagesh
APPLICANT: Marchionni, Mark A.
                                                                                                                                                                                                                                                                                                                               APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bermingham-McDonogh, Olivia APPLICANT: Goldin, Stanley M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GOODEARL,
                               56 SPVSVG 61
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SPVSVG
                                                                 Conservative
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                                                                                 100.0%;
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                                                                               7.6%; Score 6; I
100.0%; Pred. No.
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                                                               Mismatches
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                                                                                 DB 4;
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                                                               0;
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RESULT 15
US-09-715-021-49
US-09-715-021-49
US-09-715-021-49
US-09-715-021-49
US-09-715-021-49
PATECANT US-014377
GENERAL INFORMATION:
APPLICANT: GENERAL, ANDREW
APPLICANT: GENERIELD, MICHAEL
APPLICANT: MINGHETIL, LUISA
APPLICANT: MINGHETIL, LUISA
APPLICANT: MINGHETIL, LUISA
APPLICANT: MINGHETIL, LUISA
APPLICANT: MINGHERI LUISA
APPLICANT: MINGHERI LUISA
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APPLICANT: MINGHERI LUISA
APPLICANT: MINGHERI LUISA
APPLICANT: MINGHERI LUISA
APPLICANTION NUMBER: 05/08/735,021B
CURRENT FILING DATE: 1996-10-22
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 07/965,173
EARLIER APPLICATION NUMBER: 07/965,173
EARLIER APPLICATION NUMBER: 07/965,173
EARLIER APPLICATION NUMBER: 07/965,173
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EARLIER FILING DATE: 1992-00-03
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
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length: 2000000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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      61
215
824
880
906
906
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688
777
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1147
1131
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1168
238
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                               10 US-09-746-491-48
10 US-09-864-761-45510
10 US-09-864-761-415510
10 US-09-755-109-21
10 US-09-764-887-226
10 US-09-764-887-226
10 US-09-764-869-1118
10 US-09-764-869-798
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10 US-09-784-8761-38224
                                                                                                                                                                                                                                    US-10-001-876-210
US-09-909-567B-53
US-09-893-519A-36
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                      US-10-024-579-16
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Compugen Ltd
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Sequence 4740, A
Sequence 210, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 415, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 216, App
Sequence 1118, App
Sequence 1118, App
Sequence 1798, App
Sequence 1824, App
Sequence 148, App
Sequence 1470, Ap
Sequence 5722, Ap
Sequence 1470, Ap
Sequence 1470, Ap
Sequence 1470, Ap
Sequence 16, Appl
Sequence 1722, App
                                                                                                                                                                                                                                                                                                              Description
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7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6
323	316	310	306	299	298	290	290	290	290	290	290	290	290	290	290	290	290	290	290	283	267	267	264	264	257
9	10	9	12	9	10	12	9	9	9	9	9	9	9	9	9	9	9	9	9	12	9	9	12	10	12
US-09-984-245-160	US-09-799-777-49	US-09-975-719-11	US-10-080-644-11	US-09-808-602-63	US-09-764-853-552	US-10-040-655-7	US-10-140-002-222	US-10-143-114-222	_	US-10-140-474-222	US-10-137-865-222	10-	176-918	US-10-175-746-222	US-10-140-470-222	US-10-123-904-222	US-10-121-049-222	US-10-028-072-222	US-10-041-006A-7	US-10-024-579-10	US-09-808-602-25	US-09-808-602-23	US-10-024-579-12	US-09-848-696-4	US-10-024-579-14
Sequence 160, App	Sequence 49, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 63, Appl	Sequence 552, App	Sequence 7, Appli	-	Sequence 222, App	Sequence 222, App	Sequence 222, App	•		Sequence 222, App		Sequence 222, App	•	•	Sequence 222, App	Sequence 7, Appli	Sequence 10, Appl		Sequence 23, Appl	Sequence 12, Appl	Sequence 4, Appli	Sequence 14, Appl

ALIGNMENTS

US-09-864-761-44740

Sequence 44740,

Application US/09864761

Patent No. US20020048763A1

APPLICANT: Penn, Sharron G.

David K.

S

CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PRILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-030
PRIOR FILING DATE: 2001-030
PRIOR FILING DATE: 2001-030 TITLE OF INVENTION: HUMAN ENROME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-x-1 CURRENT APPLICATION NUMBER: US/09/864,761 Hanzel, Davidensheng

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RESULT 3
US-09-909-567B-53
; Sequence 53, Application US/09909567B
; Publication No. US20030022257A1
; GENERAL INFORMATION:
                                                                                                                                                                              Query Match
Best Local Similarity
Watches 7; Conserve
                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-876-210
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US-10-001-876-210
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; OTHER INFORMATION:
US-09-864-761-44740
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Best Local Similarity
Thehes 7; Conserve
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SEQ ID NO 210
LENGTH: 215
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                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,186
PRIOR FILING DATE: 2000-11-21
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and FILE REFERENCE: DEX-0285
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 21:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MAR TO ACO16057.3
OTHER INFORMATION: EXPRESSED IN ADJULT LIVER, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.53
OTHER INFORMATION: EXPRESSED IN BORD MARROW, SIGNAL = 0.52
OTHER INFORMATION: SWISSPROT HIT: 013563, EVALUE 2.00e+00
OTHER INFORMATION: EST_HUMAN HIT: BF570694.1, EVALUE 4.00e-16
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Liu, Chenghua
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Cafferkey, Robert
Ali, Shujath
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 Mismatches

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Pred. No.
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Pred. No.
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5.7;
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Query Match
Best Local Similarity
Thes 7; Conserve
                                                                                    US-09-893-519A-36
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CURRENT APPLICATION NUMBER: US/09/909,567B

CURRENT FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: 60/219,834

PRIOR FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 56

SOFTWARE: PatentIn version 3.1

SEQ ID NO 53

LENGTH: 824
                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 880
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TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/16548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
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APPLICANT:
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                                                                                                                                                     NAME/KEY: misc_feature
OTHER INFORMATION: Corresponds to SEQ ID NO:
PUBLICATION INFORMATION:
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                                                                                                  DATABASE ACCESSION NUMBER: Human Genbank/AAC39727
DATABASE ENTRY DATE: 1998-05-06
RELEVANT RESIDUES: (1)..(880)
                                                                                                                                                                                                                         TYPE: PRT ... ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
                                                                                                                                                                                                           FEATURE:
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Chen, Seiyu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCCOY, Melissa
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BRADLEY, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOORE, Daniel
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MENDILLO, Marc
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                                  Score 7; pred. No.
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Pred. No.
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SEQ ID NO 48
LENGTH: 906
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/746,491 CURRENT FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: No. US20020137202Alel Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 15966-621
                                                                                                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                     PRIOR
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                                                                      APPLICATION NUMBER: PCT, FILING DATE: 2001-01-30
                                                                                                              APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                               FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                 APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                 FILING DATE: 2001-01-30
                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00667
               APPLICATION NUMBER: PCT/US01/00663
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o. US20020048763A1
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Hanzel, David K.
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                                                                        2001-01-30
2001-01-30
NUMBER: PCT/US01/00665
2001-01-30
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Mismatches
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p. 75;
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US-09-755-109-21

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Best Local Similarity
"~+~hes 6; Conserv
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.66

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.63

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59

OTHER INFORMATION: EST_HUMAN HIT: BF672312.1, EVALUE 8.00e-04
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                       PRIOR APPLICATION DATA
                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/755,109
FILING DATE: 08-Jan-2001
CLASSIFICATION: 435
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DANO, KELD
                                                                                                                                                                                                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK STREET: 419 SEVENTH STREET, N.W.
                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
APPLICATION NUMBER: US/08/635,666
                                                                                                                                                                                                                                                ZIP: 20004
                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                             STATE: D.C
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MASUCCI, MARIA TERESA
APPELLA, ETTORE
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ROLDAN, ANN LOURING
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KRISTENSEN,
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o. 27;
                                                                                                                                     Version #1.25
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22-APR-1996

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Best Local :
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                                                                                                                                  PRIOR PRIOR
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 21:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 QPGPAH 13
                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                    FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                       FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 24263.6
APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                   FILING DATE: 2001-01-30
                                                                                             APPLICATION NUMBER: PCT/US01/00664
                                                                                                              FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 07/334,613
FILING DATE: 07-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 34 amino acids
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FILING DATE: 06-DEC-1991
APPLICATION NUMBER: WO PCT/DK90/00090
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Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David K.
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06-OCT-1994
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                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2
SEQ ID NO 226
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-09-764-887-226
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APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA113
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 226, Application Patent No. US20020042096A1
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                                                                      Matches
                                                                                                     Query Match
                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                    Prior application data removed - NUMBER OF SEQ ID NOS: 658 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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OTHER
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ORGANISM: Homo sapiens
                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                          NAME/KEY: SITE LOCATION: (6)
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28
                                 55 ISPVSV 60
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les 6; Conserv
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ISPVSV 33
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N: EXPRESSED IN PLACENTA, SIGNAL = 2.6
N: EXPRESSED IN HEART, SIGNAL = 3.2
N: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
N: EXPRESSED IN LUNG, SIGNAL = 3.7
N: EXPRESSED IN HELA, SIGNAL = 3.7
N: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9
N: EXPRESSED IN FORMARROW, SIGNAL = 2.
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Pred. No.
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US-09-864-761-35919
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Best Local Similarity
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PI
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APPLICATION NUMBER: PCT/US01/00664
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APPLICATION NUMBER: PCT,
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EXPRESSED IN HELA, SIGNAL = 3
EXPRESSED IN PLACENTA, SIGNAL = 4.2
EXPRESSED IN HEART, SIGNAL = 4.2
EXPRESSED IN BRAIN, SIGNAL = 3.7
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7.6%;
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Score 6;
Pred. No.
                                                                                                 IN BONE MARROW, SIGNAL = 3.7
IN LUNG, SIGNAL = 3.8
IN BT474, SIGNAL = 2.9
IN FETAL LIVER, SIGNAL = 3.7
IN ADDLT LIVER, SIGNAL = 3.7
                                                                                    R09295.1,
  DB 10;
5. 66;
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US-09-764-869-798
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SEQ ID NO 1118
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 798, Application US/09764869 Patent No. US20020061521A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 798
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Best Local
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                                                                                                                                              FEATURE:
NAME/KEY: SITE
LOCATION: (56)
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                             Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
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NAME/KEY: SITE
LOCATION: (4)
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                                                                                                                                                                                                  LENGTH: 93
TYPE: PRT
ORGANISM: Homo sapiens
                                               OTHER INFORMATION:
                                                              NAME/KEY: SITE LOCATION: (79)
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                                                                                                         NAME/KEY: SITE LOCATION: (60)
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LOCATION: (48)
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                               NAME/KEY: SITE
                 LOCATION:
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                        SEQ ID NO 38224
LENGTH: 114
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                  OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                   FEATURE:
                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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              EXPRESSED IN ADULT LIVER, SIGNAL = 1
EXPRESSED IN HEART, SIGNAL = 0.86
SWISSPROT HIT: P08503, EVALUE 2.70e-01
EST_HUMAN HIT: AV703581.1, EVALUE 2.10e+00
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US-09-764-847-828
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Best Local Similarity
Whithes 6; Conserve
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Patent No. US20020132767A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 828
LENGTH: 147
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Best Local Similarity
Matches 6; Conserv
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                                                                      Query Match
Best Local :
                                                           Matches
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CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                          Prior application data removed - NUMBER OF SEQ ID NOS: 2003
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                                                                                                                                               LENGTH: 14
TYPE: PRT
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108 LLPRPA 113
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les 6; Conserv
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                          5 LLPRPA 10
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Search completed: March Job time: 4.33133 secs

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               March 4, 2003, 12:36:41; Search time 53.8474 Seconds (without alignments) 1036.856 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed D

SUMMARIES

10	9	8	7	6	ഗ	4	ω	۸	1	Result No.
340	340	340	340	340	340	340	340	340	340	Score
81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	Query Match Length DB
1200	919	919	782	712	712	653	653	645	645	Length
21	23	21	18	23	21	23	21	22	22	80
AAB21208	AAM51148	AAB21203	AAW19764	AAM51149	AAB21204	AAM51145	AAB21200	AAB61593	AAB60408	ID
Human HER-2/neu pr	Her-2/neu extracel	Human HER-2/neu fu	Her2-GM-CSF immuno	Her-2/neu extracel	Human HER-2/neu fu	Human Her-2/neu on	Extracellular HER-	Human ErbB2 extrac	Human ErbB2 oncopr	Description

45	1.4	43	42	41	40	39	38	3 7	36	35	34	<u>ა</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
ä	8 3	83	83	86	96	166	166	166	187	191	191	191	289	292	292	292	292	292	307	319	340	340	340	340	340	340	340	340	340	340	340	340	340	340
	19.8	•	•	•	•	•	•	•	•	•		•	•	•	69.7	•	69.7		•	76.1	٠	•	81.1	81.1	•	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1
419	419	419	419	624	97	166	166	166	1433	191	191	191	289	. 697	690	564	555	479	1223	951	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255	1255
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AAE09202	\sim	1	AAE09181	AAR08222	AAW00327	AAB48763	07	34	AAR39568	8	AAY14572	ū	AAE13120	AAE13111	AAE13109	AAE13110	AAE13108	AAE13112	92	9	AAU74545	AAU77114	AAM51143	AAE20479	AAE24067	AAB60167	· AAG88267	AAB85458	AAE12130	AAY92620	AAY84780	AAB21198	AAW92406	AAW01111
Human p68HER-2 gen	2	p68HER-2	Human p68HER-2 gen	\sim	HER - 2/n	ErbB2	protei	Human ErbB2 domain	nce of		erbB2 recep	ErbB2 prote	e human HER-	HER500-rGM-	HER500-hGM	HER500 fus	HER500 fusi	HER300-	breast canc	Fv-erbB2EC f	HER2 (ErbE	Her-2/neu	Her-2/neu	Her-2/neu p	n Her-2 pr	transgene pl	neu amino a	۵	Human tyrosine kin	hereg	acid seque	HER-2/neu		HER-2/neu protein.

ALIGNMENTS

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RESULT 1
AAB60408
AAB60408;
                         AAB60408 standard; Protein; 645 AA.
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colorectal cancer; non-small cell lung cancer; metastatic breast cancer; affinity purification. Anti-ErbB2 monoclonal antibody 2C4; HER2; mouse; murine; humanised; VL; light chain variable region; cancer; cytostatic; EGFR-expressing cancer epidermal growth factor receptor; colon cancer; metal cancer; tumour; colorectal cancer; non-small cell lung cancer; metastatic breast cancer

Human ErbB2 oncoprotein, SEQ ID NO:13.

24-APR-2001

(first entry)

WO200100245-A2 Homo sapiens.

23-JUN-2000; 2000WO-US17366

04-JAN-2001.

25-JUN-1999; 99US-0141316

(GETH) GENENTECH INC

CW, Presta LG, Sliwkowsky 3

WPI; 2001-080862/09

Treating cancer in a human, where the cancer expresses epidermal growth

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                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising such nucleic acids; the recombinant production of a humanised CErbB2-binding antibody; and an immunoconjugate comprising a humanised cC ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies act by antagonising ErbB receptors, and as inhibitors of transforming CC growth factor alpha (TGF-alpha)-activated mitogen activated protein CC kinase (MAPK). The method of the invention is used for treating cancer, cespecially colon cancer, rectal cancer, colorectal cancer (especially colon cancer, rectal cancer, colorectal cancer (especially con-small cell lung cancer), or breast cancer (especially CC metastatic breast cancer). The antibodies may also have non-therapeutic CC uses e.g., as affinity purification agents. Using an antibody which binds CC drugs, as EGFR is also highly expressed in other tissues such as the CC liver and skin, where the active drug will also bind, with skin toxicity CC having been observed for EGFR-targetted drugs. Antibodies which bind CC ErbB2 are anticipated to have a better safety profile than such drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for treating cancer in a human patient, wherein the cancer expresses epidermal growth factor receptor (EGFR), comprising administering an antibody which binds ErbB2 (HER2; AAB60408).
                                                                                  Human ErbB2 extracellular domain.
                     antibody;
                                                                                                                           04-APR-2001
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                                           Human; ErbB2;
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                                                                                                                                                                                                                                                                                                                                                          YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340
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                       ErbB
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               cytostatic; prostate cancer; receptor tyrosine kinase; B receptor; monoclonal antibody 2C4; variable light cha
                                                                                                                                                                                                           protein;
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                                                                                    AAB21200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                                                                                                                                                          YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340
                                                                                                                                                                                                                                                                                                                                DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                                                                                                                                                                                                                                                                                                                                         ELTYLFTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                                                                         YNYLSTDYGSCTLYCPLHNQEVTAEDGTQRCEKCSKPCAR
                                                                                                                                                                                                                    AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                              AAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                          LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                       LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scher HI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0141315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer in a human and blocks ligand
                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sliwkowski MX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%;
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                                                                                    653 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 340; DB 22; Pred. No. 3.9e-302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises administering an antibody activation of an ErbB receptor -
                                                                                                                                                           340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Extracellular HER-2/neu protein.

12-JAN-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the extracellular HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheever MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-505976/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HER-2/neu; oncogene; tyrosine kinase; cytostatic; breast cancer; prostate cancer; ovarian cancer; lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                          these neoplasias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1999;
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301
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                                                                                                                                                                                                                                                                                                                 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                                                                                               LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
           YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340
                                                       AAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                            DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                                                                                                                                                                                                         ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                    AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                                                                                                                                            DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                       ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                                  MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 9; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                             653 AA;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0117976
                                                                                                                                                                                                                                                                                                                                                                            81.1%; Score 340; DB 21; 100.0%; Pred. No. 4e-302;
                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                            Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 4 AAM51145

Вb QΥ

1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL

60

Matches

Local

Similarity

81.1%; ilarity 100.0%; Conservative (

0;

Mismatches

0,

0;

Gaps

0;

Score 340; DB 23; Pred. No. 4e-302;

Length 653;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine, or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in
                                                                                                                                                                                                                                                         of receptor-like glycoproteins. It comprises an extracellular domain with homology to the epidermal growth factor receptor (EGFR), a highly hydrophobic transmembrane domain and a C-terminal intracellular domain that also shows homology to EGFR. Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and vaccines comprising the fusion proteins or nucleic acid melecules. In preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of the extracellular domain of human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic self-protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu (see AAM51143) is a member of the tyrosine kinase family
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Her-2/neu fusion protein for treating or preventing cancer by eliciting or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 9; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Her-2/neu; oncogene; cancer; tumour; vaccine; human;
tyrosine kinase; receptor; c-erbB2; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Her-2/neu oncoprotein extracellular domain
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                  to
                                    inhibit the development of cancer in a patient.
653 AA;
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100.0%;

Pred. No. 4.3e-302;

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RESULT 5
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                       The present sequence is a fusion protein comprising the extracellular domain and a preferred portion of the phosphorylation domain of the human HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. They may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias.
                                                                                                                                                                                                                        {\tt HER-2/neu} extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                                                              (CORI-)
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                                                                                                                                                                                  Claim 27; Fig 13; 128pp; English.
                                                                                                                                                                                                                                                                                                    Cheever MA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human HER-2/neu fusion protein
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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Query Match

81.18;

Score

340;

DB 21;

Length 712;

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RESULT 6
AAM51149
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                                                         or enhancing an immune response to the protein, has He extracellular domain fused to Her-2/neu intracellular phosphorylation domain
The present sequence is that of a fusion protein extracellular domain and a fragment (DeltaPD) of
                                  Claim 37; Fig 13; 141pp; English
                                                                                 Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu
                                                                                                                                             Cheever
                                                                                                                                                                  (CORI-)
                                                                                                                                                                                                                           03-AUG-2001; 2001WO-US24283
                                                                                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM51149 standard;
                                                                                                                    WPI; 2002-241743/29
                                                                                                                                                                                                     03-AUG-2000; 2000US-0632507
                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                               Her-2/neu extracellular domain-delta-phosphorylation
                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                       Her-2/neu;
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eptor; c-erbB2; gene therapy.
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Matches 340;
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656..782
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12-JAN-2001
                                                  AAB21203;
                                                                                                   AAB21203 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APC that activates response - can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruegg CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              782 AA;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctivates T-cells to give multivalent cellular can also induce a cytotoxic T-cell response
                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu
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100.0%;
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                                                                                                   919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 340;
Pred. No.
                                                                                                   ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Human

HER-2/neu

fusion protein.

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Query Match
Best Local S
Matches 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 12; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt HER-2/neu} extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheever MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colon cancer; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2000; 2000WO-US02164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast cancer;
                                                                                                                                                                                                                                                                                                                              121
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301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                                       DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                                                                                                                                                                                          LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                      YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340
                                                                                                        AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                           DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                    ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                                                                                                                                                                                                   LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HER-2/neu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORIXA CORP.
SMITHKLINE BEECHAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0117976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine kinase; cytostatic; vaccine; cer; ovarian cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 340; DB 21;
Pred. No. 5.3e-302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 919;
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1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL

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340;

Local

Similarity

Conservative

0;

Mismatches

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0;

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Score 340;

DB 23;

Length Indels

919;

Pred. No. 5.3e-302;

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RESULT 9
AAM51148
vaccines comprising the fusion proteins or nucleic acid molecules. Con preferred fusion proteins, the extracellular domain of a Her-2/neu protein is fused to a Her-2/neu intracellular domain or phosphorylation domain (or its DeltaPD fragment). An immune response to Her-2/neu protein is elicited or enhanced by administering the fusion protein in the form of a vaccine; or by transfecting cells of an animal ex vivo with a nucleic acid encoding the fusion protein, and delivering the transfected cells to the animal. The fusion proteins, nucleic acids, and isolated specific T-cells are useful for inhibiting the development of a cancer, especially breast, ovarian, colon, lung or prostate cancer in a patient. The cells that specifically react with a Her-2/neu fusion protein can be used to remove tumour cells from a sample in corder to inhibit the development of cancer in a patient.
                                                                                                                                                                                                                                                                    The present sequence is that of a fusion protein between the extracellular domain and phosphorylation domain of human Her-2/neu (see AAM51143), an oncogenic self-protein and target for anti-cancer vaccines. The fusion protein can be obtained by recombinant DNA methods. Her-2/neu overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins, nucleic acids encoding them, viral vectors, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylation domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheever MA, Gheysen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000; 2000US-0632507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Her-2/neu extracellular domain-phosphorylation domain fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-241743/29
                                                                                                                                                                                                                                                                                                                                                                                                          2; Fig 12; 141pp; English
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SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oncogene; cancer; tumour; vaccine; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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654..919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                    The present sequence is the human HER-2/neu protein. It is a member of the tyrosine kinase family of receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGRR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and
                                                                                                                                                                                                                 {\rm HER}\text{-}2/{\rm neu} extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and prostate cancers -
                           to treat malignancies such as breast, ovarian, prostate cancers, and may be used as an antige
                                                                                                                                                                                     Disclosure; Fig 15; 128pp; English.
                                                                                                                                                                                                                                                                                                                      Cheever MA,
                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.

(SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast cancer;
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                                                                                                                                                                                                                                                                                           2000-505976/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-2/neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
cancer; prostate cancer; ovarian cancer; lung cancer;
                                                                                                                                                                                                                                                                              AAA89736
                                                                                                                                                                                                                                                                                                                     Gheysen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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                           an antigen to vaccinate against
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RESULT 11
AAW01111
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                                                                                                                                                                                                                                                                                        HER-2/neu; c-erbBl; pl85; oncogene; tyrosine protein kinase; breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer; immunisation; tumour; vaccine; vector.
                                     DNA encoding treatment of
                                                                                                                                                                                                                                                    Key
        Claim
                             associated
                                                                    N-PSDB;
                                                                              WPI; 1996-455361/45
                                                                                                  Cheever MA,
                                                                                                                                        31-MAR-1995;
                                                                                                                                                                               03-OCT-1996
                                                                                                                                                                                                    WO9630514-A1
                                                                                                                                                                                                                                                                                                                                                         01-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                AAW01111 standard; Protein; 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                    (UNIW )
                                                                                                                                                            28-MAR-1996;
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             AAW01111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
        2; Page 56-61;
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                                                                    AAT40739
                                                                                                                     VIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                    HER-2-neu poly:peptide(s) - used for \rm I malignancies with which the HER-2/neu
                                                                                                 Disis ML;
                                                                                                                     WASHINGTON
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                                                                                                                                        95US-0414417
                                                                                                                                                            96WO-US01689
                                                                                                                                                                                                                                         Location/Qualifiers 676..1255
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                                                                                                                                                                                                                      /label= Intracellular_domain
/note= "claimed domain, usef
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       71pp; English
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Pred. No.
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    used for prevention

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6.6e-302;
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                                     oncogene
                                                                                                                                                                                                                       immunisation'
                                   or
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RESULT 12
AAW92406
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Best Local :
                                  01-APR-1996;
17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is the product of the HER-2/neo oncogene (see also AAM40739). The protein is over-expressed in various cancers, including breast, ovarian, colon, lung and prostate. The intracellular domain of the protein can be used to immunise an animal against a malignancy with which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector
                                                                                                                                                                                                                                                                                                                      21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                       AAW92406 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that directs expression of the polypeptide.
                                                                                                   01-APR-1996;
                                                                                                                            09-FEB-1999
                                                                                                                                                    US5869445-A
                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                      malignancy;
          (UNIW ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                     YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340;
                                                                                                                                                                                                                                                                                          HER-2/neu oncogene protein.
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                                                                                                                                                                                                                                                                  oncogene; immune response;
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                                                                                                                                                                                                                                                         treatment; tumour
           WASHINGTON
                                                                                                                                                                                                                                                                                                                      (first
                                  96US-0625101.
93US-0033644.
93US-0106112.
95US-0414417.
                                                                                                  96US-0625101
                                                                                                                                                                                       Location/Qualifiers 676..1255
                                                                                                                                                                                                                                                                                                                                                                       Protein;
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100.0%;
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Pred. No. 6.
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                                                                                                                                                                                                                                                                    cell;
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                                                                                                                                                                             immune
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                                                                                                                                                                                                                                                                    cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                    immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 13
AAB21198
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Best Local S
Matches 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human HER-2/neu oncogene protein. A fragm of this protein is used in a method for eliciting or enhancing an immu response to HER-2/neu protein. The polypeptide can stimulate T cells a B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
                                                                                                                                            human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
breast cancer; prostate cancer; ovarian cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preventing tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheever MA,
29-JAN-1999;
                        28-JAN-2000; 2000WO-US02164
                                                   03-AUG-2000
                                                                                                                                                                                                                                                                   AAB21198 standard; protein; 1255
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                                                                             WO200044899-A1
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99US-0117976
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Pred. No. 6.9e-302;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HER\mbox{-}2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and prostate cancers -
          SPLICE erbB-2 receptor protein; cell transformation disorder; tumor cell proliferation; tissue degeneration; arthropathy; bone resorption; inflammatory disease; degenerative disorder; wound healing.
                                                                                                         08-AUG-2000
                                                                                                                                                                 AAY84780 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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)B; AAA89736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%; Score 340; DB 21; 100.0%; Pred. No. 6.9e-302;
                                                                               the
                                                                               SPLICE
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                                                                          erbB-2 receptor protein
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RESULT 15 AAY92620 ID AAY92

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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N-PSDB; AAA14812.
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YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR
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Pred. No. 6.9e-302;
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                          /label= insertion_region
/note= "sultable for foreign epitope insertion
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/note= "suitable for foreign epitope insertion"
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/note= "suitable for for
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YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR

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AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC

181 181 121 121 61 61

LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC

240

240

180 120

180

DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA

DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA

ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG

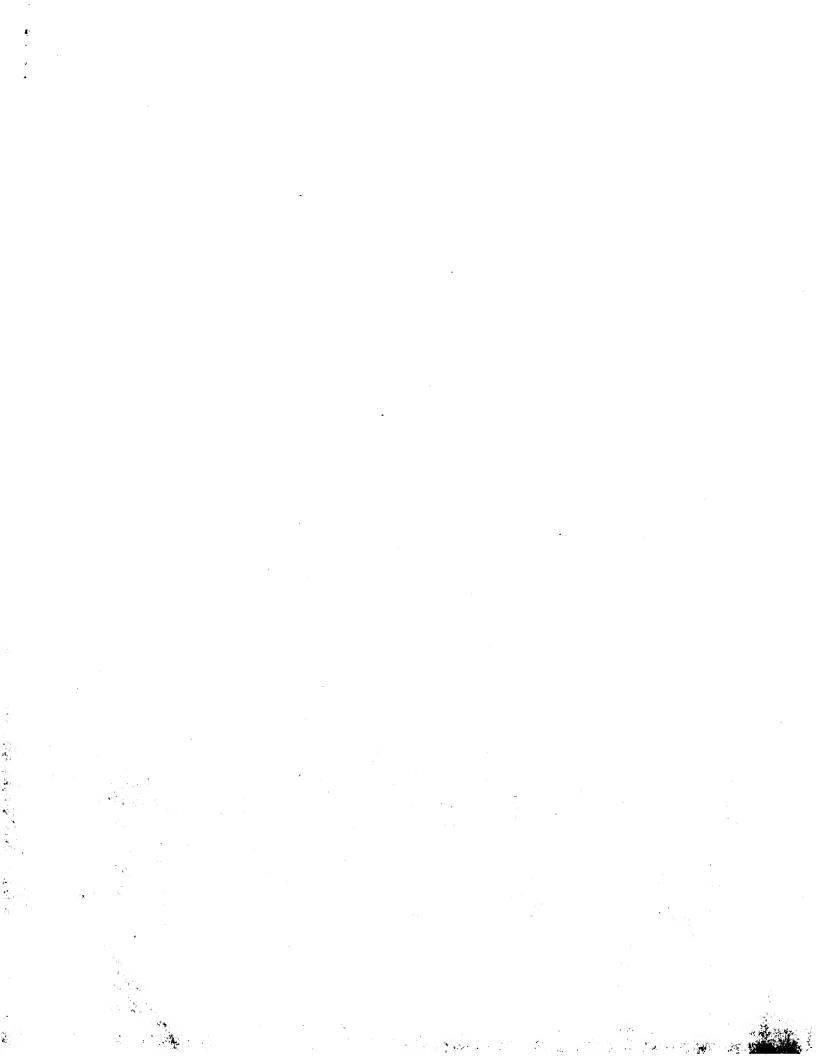
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL

MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL

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PD XX PD XX PD XX PF PR XX PR PR XX XX PF I
Query Match
Best Local
                                                                                                            producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGFBB comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer
                                                                                                                                                                                                                                                                  response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign T helper epitopes were identified (see features table). The method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA09455
                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-349917/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1998;
20-OCT-1998;
                                                                                                when the PA is human PSM, FGF8b and Her2, respectively.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 is the human heregulin 2 (Her2) sequence. Immunogenic analogues can be used in the claimed method as an autovaccine to induce a
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Birk P, Karlsson
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98US-0105011
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                                                            AA;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               claimed method as an autovaccine to induce
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Pred. No. 6.9e-302;
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                  Length 1255;
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Search completed: March 4, 2003, 12:44:57 Job time : 57.8474 secs



5.1.3

Run on: March 4, 2003, 12:43:27 ; Search time 47.1165 Seconds (without alignments

854.910 Million cell updates/sec

Perfect score: US-09-234-208B-2

MELAALCRWGLLLALLPPGA....VGRGPDPDAHVAVNLSRYEG 419

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_73:*

pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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מאט-מוומומן למסרפו	DOLLER C GCCCItcia	cerine O-acetyltra	hypothetical prote	thiol, disulfide in	thiol disulfide in	hypothetical prote	endonuclease III -	glycosyltransferas	type III export pr	trans-activating t	heme exporter prot	stromal cell-deriv	fibroblast growth	trypsin inhibitor	hypothetical prote	capsular polysacch

ALIGNMENTS

C;Species: Homo sapiens (man) C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999 C;Accession: A24571; A25491; A44188; B44188; I59509; I57622 protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N; Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e

R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growt A;Reference number: A24571; MUID:86118663; PMID:3003577 A; Reference number: A; Accession: A24571

A;Molecule type: mRNA
A;Residues: 1-1255 </AN>
A;Residues: 1-1255 </AN>
A;Residues: 1-1255 </AN>
A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
A;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid A;Reference number: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491

A; Molecule type: DNA A; Residues: 737-1031 <SEM>

A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to A;Reference number: A44188; MUID:86070181; PMID:2999974
A;Accession: A44188 PID:g553282 A.; McGrath, McGrath, J.; Seeburg

EGF receptor shares chro

A; Molecule type: DNA A; Residues: 740-910 <COU1>

A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989

A; Accession: B44188

A;Molecule type: mRNA A;Residues: 1-517,'RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2> A;Cross-references: GB:M11730; NID:g183986

A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma. A;Reference number: 159509; MUID:85272597; PMID:2992089
A;Reference number: 159509; MUID:85272597; PMID:2992089 R:King, C.R.; Kraus, M.H.; Aaronson, S.A. Science 229, 974-976, 1985

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 832-909 < REX>

A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptio
A;Reference number: 157622; MUID:87286898; PMID:3039351 A; Reference number: A; Accession: I57622

A; Status: translated from GB/EMBL/DDBJ

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Fig. 1.2. // Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
Fig. 1.2. // Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
Fig. 1.2. // Product: Extracellular #status predicted <EXT>
Fig. 1.2. // Product: EGF receptor extracellular domain repeat <EE1>
Fig. 1.2. // Product: EGF receptor extracellular domain repeat <EE1>
Fig. 1.2. // Product: EGF receptor extracellular domain repeat <EE2>
Fig. 1.2. // Product: EGF receptor extracellular domain repeat <EE2>
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Fig. 1.2. // Product: EGF receptor extracellular domain repeat <EE1>
Fig. 1.2. // Product: EGF receptor extra
                                                                                                                                                                                              Gene 140, 251-255, 1994
A; Title: Cloning and activation
A; Reference number: I48161; MUII
A; Accession: I48161
A;Cross-references:
C;Genetics:
A;Gene: neu
                                                                                                                                                                                                                                                                                                                                                                 p-185 precursor - golden hamster
c;Species: Mesocricetus auratus (golder
C;Date: 02-Jul-1996 #sequence_revision
C;Accession: I48161
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C; Function:
A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue
C; Superfamily: epidermal growth factor receptor; protein kinase homology
                                                                                                 A; Molecule type: mF
A; Residues: 1-1254
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A; Introns: 25/1; 75/3; 147/1; 883/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Mesocricetus auratus (golden hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GDB:120613;
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                                                                                                                                                               Status: preliminary; translated
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251-255,
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                                                              GB:D16295; NID:g493236; PIDN:BAA03801.1; PID:g747595
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                                                                                                                                                                                                                                                                                                                              Y.; Nagao, M.;
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                                                                                                                                                                                                                                                                                                                                  Arai, M.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                             proto-oncogene
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C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequer C;Accession: B82252 R;Heidelberg, J.F.; Eisen,

RnfE-related protein VC1012 [imported] - Vibrio cholerae

#sequence_revision

20-Aug-2000 #text_change

(strain N16961 serogroup O1)

02-Feb-2001

J.A.; 1.D.; V

; Nelson, W.C.; Vamathevan, J.;

Clayton, R.A.; Bass, S.; Qin,

n, M.L.; Dragoi,

Dodson, R.

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C;Superfamily: epic
C;Keywords: ATP
F;718-983/Domain: F
F;726-734/Region: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Nolecule type: mRNA
A; Residues: 1-1260 <BAR>
A; Cross-references: EMBL:X03362; NID:g56745; PID:
                                                                                                                                                            F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;731,191,263,535,576,634/Binding atTP-binding motif
F;751,191,263,535,576,634/Binding atTP-binding with (Asn)
F;691/Binding site: phosphate (Thr) (covalent) #status pre
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #
                                                                                                                                                                                                                                                                                                            C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphore;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Carcinogenesis 12, 1975-1978, 1991
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane 2-thiazolyllformamide or N-methyl-N-nitroscurea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 637-663, 'V', 665-702 <MAS>
A; Note: authors translated the codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
    B
                                                                                                                                                                                                                                                                         F;20-1260/Product: protein-tyrosine kinase neu *status predicted F;558-680/Domain: transmembrane *status predicted <TMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: A24562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: The neu oncogene encodes an epidermal g
A; Reference number: A24562; MUID:86118662; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Bargmann, C.I.; Hung, M
Nature 319, 226-230, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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Best Local
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231
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protein
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                                                                                                 12.4%;
100.0%;
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kinase
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ATP-binding
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Pred. No.
                                                                                                 Score 52;
Pred. No.
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                                                                                                                                                        (Tyr) (covalent) #status
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                                                                                                 DB 1; L, 6.2e-43;
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A;Cross-references: GB:M37394
C;Superfamily: epidermal grow
C;Keywords: alternative splic
                                                                                                                                                               Mol. Cell. Biol. 10, 2973-2982, 1990
Mol. Cell. Biol. 10, 2973-2982, 1990
A;Title: A truncated, secreted form of the epidermal growth factor receptor is
                                                                                                                                                                                                                                                            epidermal growth factor receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Oct-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: sequence extracted from NCBI backbone (NCBIN:76892, NCBIP:76893) C; Superfamily: epidermal growth factor receptor; protein kinase homology C; Keywords: ATP; growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-527 <FLI>
A;Cross-references: GB:M77637; NID:g211737; PIDN:AAA48759.1; PID:g211738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A42032; MUID:92123214; PMID:1732751 A;Accession: A42032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epidermal growth factor receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
                                                                                                              A; Molecule type: mRNA
A; Residues: 1-644 <PET>
                                                                                                                                                                                                                              R; Petch, L.A.; Harris,
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C; Superfamily: conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A82035; A; Accession: B82252
                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                 C; Accession: A36325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l, R.R.; Mekalanos, J.J.;
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                      Superfamily: epidermative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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9; Conserv
            Similarity
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9; Conser
                                                                         epidermal growth factor receptor; protein kinase homology
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ilarity 100.0%;
Conservative
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                                                             splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor factor receptor
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            2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter, J.C.; Fraser,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE003852; NID:g9655473; O1; strain N16961; biotype
          Score
Pred.
                                                             ATP;
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e 9;
No
                                                             growth
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5. 0.82;
        DB . 2;
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                            Length 644
                                                                                                                                                                                                                                A.; Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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R:Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 265, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672;
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                                                                                                                                                                                                                                                                                                                                       A;Residues: RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA',307-798-799,'Tp',802-811,'R',813-942 <XUY>
A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF re R;Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, Science 224, 843-848, 1984
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A;Title: Characterization and sequence of the promoter region A;Reference number: A25772; MUID:85270438; PMID:2991899
A;Accession: A25772
A; Accession: A23062
                                A; Reference number: A23062;
                                                                A;Experimental source: epidermoid carcinoma cell line A431 R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, Biochem. Biophys. Res. Commun. 124, 125-132, 1984
                                                                                                                                                                       A; Residues: 713-964 <LIN>
                                                                                                                                                                                                                                          A; Accession: A43615
                                                                                                                                                                                                                                                                       A; Title: Expression cloning of human EGF receptor complementary A; Reference number: A43615; MUID:84196372; PMID:6326261
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A; Residues: 1-29 <HAL>
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A; Residues: 1-29 <HA2>
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A; Residues: 1-29 <ISH>
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A;Note: the authors translated the codon AAG for residue 540 as Asn
R;Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
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Residues: 1-1210 <ULL>
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epidermat growth structure (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
     Oncogene 6, 673-676, 1991
A;Title: Comparison of EGF receptor sequences as a guide to
A:Reference number: A43818; MUID:91232866; PMID:2030916
                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1210 <LUE>
A; Cross-references: GB: U03425
R; Avivi, A; Lax, I; Ullrich, A;
Oncogene 6, 673-676, 1991
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A;Map position: 7p12.3-7p12.1
C;Superfamily: epidermal growth factor receptor; protein kinase homology C;Superfamily: autophosphorylation; duplication; glycoprotein; phosphorylation; comparing the signal sequence #status predicted <SIG>F;1-24/Domain: signal sequence #status predicted <MAT>F;25-1210/Product: EGF receptor #status predicted <MAT>F;25-645/Domain: extracellular #status predicted <EXT>F;75-300/Domain: extracellular #status predicted <EXT>F;75-300/Domain: EGF receptor extracellular domain repeat <EE1>F;390-600/Domain: EGF receptor extracellular domain repeat <EE2>F;646-668/Domain: transmembrane #status predicted <TMM>F;646-668/Domain: transmembrane #status predicted <TMM>F;6468/Domain: transmembrane #status predicted <TMM>F;6468/Domain: transmembrane #status predicted <TMM>F;6468/Domain: transmembrane #status predicted <TMM>F
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Cell 59, 33-43, 1989
A; Title: Functional independence of the epidermal growth A; Reference number: A3331; MUID:90003233; PMID:2790960
A; Contents: annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation; internalization signal annotation signal annotation; internalization signal annotation signal signal signal annotation signal annotation signal annotation signal annotation signal annotation signal annotation signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal signal sig
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A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.
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A; Residues: 25-30,'S; 32-51,454-467 <WEB>
R; Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
J. Biol. Chem. 260, 5205-5208, 1985
A; Title: Identification of residues in the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: The mouse waved-2 phenotype results from a point mutation A; Reference number: A53183; MUID:94170986; PMID:8125255
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Nature 309, 270-273, 1984
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A; Residues: 740-744, 'X', 746-747 < RUS>
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Science 224, 294-297,
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18-726/Region: protein kinase ATP-binding mo
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9; Conserv
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Pred. No.
                                                                                                                                                                                              Schlessinger, J.; Givol,
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                                                                                          study the ligand
                                                                                                                                                                                                    D.; Morse,
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                                                                                          sit
                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Gallus gallus (chicken)
C; Date: 28-Feb-1986 #sequence_revision
C; Accession: A27720; A00643
A; Cross-references: GB:M20386
                                     A; Molecule type: ml
A; Residues: 1-1223
                                                                                                                                         A; Reference number: A27720; A; Accession: A27720
                                                                                                                                                                                                                                         R;Lax, I.; Johnson, A.; Howk; R.; S
Mol. Cell. Biol. 8, 1970-1978, 1988
A;Title: Chicken epidermal growth f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epidermal growth factor receptor precursor - chicken N; Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
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mRNA

MUID:88261272;

factor (EGF) receptor:

PMID: 3260329

Sap,

J.; Bellot, F.; Winkler, 05-May-1995 #text_change

M.; Ullrich, 04-Feb-2000

A.; Venr

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R;Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylate A;Reference number: A28941; MUID:88330814; PMID:3138233
A;Accession: A28941
                                                                                                                                                                                                                                                                   F;712-977/Domain: protein kinase homology <KIN>
F;720-728/Region: protein kinase ATP-binding motif
F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F;697.1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status ex
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G;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor; kinase-related transforming pro
E;1-24/Domain: signal sequence #status predicted <SIG>
E;648-670/Domain: transmembrane #status predicted <TMM>
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A;Residues: 1-971,'K',973-1210 <VER>
A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55587.1; PID:g488831
A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55587.1; PID:g488831
A;Paria, B.C.; Das, S.K.; Andrews, G.K.; Day, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A;Title: Expression of the epidermal growth factor receptor gene is regula A;Reference number: I49643; MUID:93126380; PMID:7678348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-10
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
submitted to the EMBL Data Library, April 1994
В
                                                                                                                                                                                                                                      F;1197/Binding
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A; Residues: 12-20,22-132 <RES>
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A; Accession: S45325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: Z12608
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A; Residues: 969-971, 'K', 973-1115, 'D'
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A; Residues: 1-714 <AVI>
                                                                                                                                                                                Query Match
                                                                                                                         Matches
                                                         239 QCAAGCTGP 247
                                                                                                                                                   Local
                                                                                                                      Similarity 9; Conser
                                                                                                                                                                                                                                      site: phosphate (Tyr) (covalent) #status experimental
                                                                                                                         Conservative
                                                                                                                                                2.1%;
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                                                                                                                                                                                                                                                                                                                                experimental
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R; Nilsen, T.W.; Ma Cell 41, 719-726,

L.B.;

Raines,

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A; NoLecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-140, 'GM', 143, 'R', 145-235, 'T', 237-238, 'E', 240-277 <AOK>
A; Cross-references: DDBJ:D89069; NID:g1906811; PIDN:BAA19007.1; PID:GC:Comment: This enzyme is a cytosolic, monomeric oxidoreductase that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;192,650/Binding site: phosphate (Thr) (covalent) (by recent) (by autophosphorylation) #state; F;54/Active site: Lys #status predicted
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #state; 1100,1183,1208/Binding site: phosphate 
    A;Gene: iCR
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                     R; Aoki, H.; Okada, T.; Mizutani, T.; Numata, Y.; Minegishi, Biochem. Biophys. Res. Commun. 230, 518-523, 1997
A; Title: Identification of two closely related genes, induc. A; Reference number: JC5284; MUID:97167735; PMID:9015353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X84349; NID:g666086; PIDN:CAA59088.1; PID:g666 R;Toft, E.; Soederstroem, M.; Ahlberg, M.B.; DePierre, J.W. Biochem. Biophys. Res. Commun. 201, 149-154, 1994 A;Title: A novel 34kDa glutathione-binding protein in mature rat ovary. A;Reference number: PC2159; MUID:94256971; PMID:8198567 A;Accession: PC2334 A;Residues: 104-121, X',123-134, 'D',136-137, 'H' <TOF>
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F:81-307/Domain: EGF receptor extracellular domain repeat <EE1>
F:397-610/Domain: EGF receptor extracellular domain repeat <EE1>
F:655-677/Domain: transmembrane #status predicted <TMM>
F:678-123/Domain: intracellular #status predicted <TMM>
F:719-984/Domain: protein kinase homology <KIN>
F:727-735/Region: protein kinase ATP-binding motif
F:136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent) #s
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F:1-30/Domain: signal sequence #status predicted <SIG>F;31-1223/Product: epidermal growth factor receptor #st
F:31-654/Domain: EGF receptor extracellular domain repersor-in transmembrane #status predicted <EMT>
F:655-677/Domain: EGF receptor extracellular domain repersor-in transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Contents: ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Apr-1997 #sequence_revision 18-Jul-1997 #text_change
C;Accession: S86982; PC2234; JC5284; PC2159; S52349
R;Wermuth, B.; Maeder-Heinemann, G.; Ernst, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Wermuth, B.; Maeder-Heinemann, G.; Ernst, Eur. J. Biochem. 228, 473-479, 1995
A;Title: Cloning and expression of carbonyl
                                                                                                                                                                                                                                                                         A; Accession: JC5284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: ovary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary A; Molecule type: mRNA
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C;Superfamil
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C;Genetics:
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A; Residues: 585-1223
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A; Reference number: A00643;
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on, J.D.; Umayam, L.A.; White, U.; Surrect, On, J.D.; Umayam, L.A.; White, U.; Surrect, On, T.; Hickey, E.K.; Holt, I.E.
science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.;
A;Title: Complete Genome Sequence of a virulent isolate of St.
Thereare number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome
A;Reference number: A8295
A;Accession: B8395
A;Accession: B3395
                                               A;Gene: SP0579
C;Superfamily: phenylalanine-tRNA ligase alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: C; Genetics:
                                                                                                                 A;Cross-references: GB:AE005672; PIDN:AAK74733.1; PID:g14972054; GSPDB:GN00164; TIGRA;Experimental source: strain TIGR4
                                                                                                                                                              A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                         C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision
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A; Residues: 1-341 <STO>
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R; Stover, C.K.; Pham, X.Q.;
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                                                                                                                                                   A; Residues: 1-348 < KUR>
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C;Species: Pseudomonas aeruginosa
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L.L.; Coulter
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S.L.; Lewis,
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Folger, K
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K.R.; Kas,
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M.R.;
                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                              Dougherty,
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Radune, D.; Holtzappl
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K.; L
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hypothetical protein aq_116 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000
C;Accession: C70311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Rv3130c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-U1-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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A; Molecule type: DNA
A; Residues: 1-375 <KUR>
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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Nature 392,
                                       R;Deckert,
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                                                                                                     A; Gene: aq_116 C; Superfamily: Aquifex aeolicus hypothetical protein aq_116
                                                                                                                                                C; Genetics:
                                                                                                                                                                                      A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:9819666; PMID:9537320
A;Recession: C70311
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-520 <AQE>
A;Cross-references: GB:AE000674; NID:g2982850; PIDN:AAC06482.1; PID:g2982861; GB:AE00
                                                                                                                                                                    A; Experimental source: strain VF5
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SDFL_HUMAN
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y allele- COMPLEX, 30 IS A F, TGF- Otein	ptor he ed in a	COM1; (jima N.,	12) type cell	selenomonas haemophilus saccharomyc r atp·sensi caenorhabdi homo sapien saccharomyc ovis aries ovis aries homo sapien xanthomonas homo sapien

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Pfam; PF00069; pkinase; 1.

Pfam; PF01030; Recep_Ldomain; 2.

Pfam; PF01030; Recep_Ldomain; 2.

Pfam; PF02757; YLP; 2.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00261; FU; 3.

SMART; SM00261; FU; 3.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

Transfermbrane; Glycoprotein; Multigene fami
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004019; YLP_motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES (BY SIMILARITY).

RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-655) HAS A FREQUENCY OF 0.207.

ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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TISSUE=Nerve;
MEDLINE=94193007; PubMed=7908275;
Nakamura T., Ushijima T., Ishizaka
Yamazaki Y., Ishikawa T.;
"Cloning and activation of the Syri
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15-DEC-1998 (Rel. 37, Created)
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15-JUN-2002 (Rel. 41, Last annotation
Receptor protein-tyrosine kinase erbB-
(p185erbB2) (NEU proto-oncogene) (C-er
                                                                             NCBI_TaxID=10036;
                                                                                                               Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Rodentia; Sciurogn
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                                                                                                                                                                                                                                                                                     AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                                                                                                                                                STANDARD;
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CONTRACTION (AUTOPHOSPHORYLATION (AUTOPHOSPHORYLATION (AUTOPHOSPHORYLATION (GLCNAC...)
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I -> V.
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P -> A (IN REF. 2).
W; 39E9DFDA04DCF962 CRC64;
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I -> V.
                                                                                                               Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                               PRT;
           Syrian
                                                                                                                                                          erbB-2 precursor (C-erbB-2).
                                                                                                                                                                     ation update)
erbB-2 precu
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          hamster neu proto-oncogene.";
                                  Nagao
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Probom; PDUVVVVIII 3.
SMART; SM00261; FU; 3.
SMART; SM00219; TYFKC; 1.
PROSITE; PS00107; PROTEIN
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HSSP; P11362;
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                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                  Proto-oncogene,
                                                                                                                                                                                                                                                                                                                            Pransferase;
                                                                                                                                                                                                                                                                                                                                      Pransmembrane;
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InterPro; IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein.
DTM: LIGAND-BINDING INCREASES PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
SUBUNIT: HETERODIMER WITH EACH OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140:251-255(1994).

140:251-255(1994).

FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALPHA AND AMPHIREGULIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                            PF00069; pkinase; 1.
PF00757; Furin-like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                                                                                                            PS00107; PROTEIN_KINASE_ATP; 1.
PS00109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
   e; Glycoprotein; Multigene family; Receptor; Signal; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1FGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA03801.1;
                                                                                                                                                                                                                                                                                                                  Disease
   Euk_pkinase;
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                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                             RECEPTOR PROTEIN-TYROSINE
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                                                                                                                                                                                                                     (BY SIMILARITY)
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  (AUTO-) (BY SIMILARITY).
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Matches 67
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CARBOHYD
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SEQUENCE
      ONCOGENIC and ONCOGENIC FORMS of the new protein.";
EMBO J. 11:43-48(1992).

-I- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,
ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A
POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
ALDHA AND AMPHIREGULIN.

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-I- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS.
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS A HOMODIME
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                                                                                                                               Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Newman R., Crumpton M.J., Sternberg M.J.E., Campbell "Three dimensional structure of the transmembrane reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(P185erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor
                                                                                                                                                                                   STRUCTURE BY NMR OF 650-668
                                                                                                                                                                                                                      expressed in the vertebrate nervous
                                                                                                                                                                                                                                                                    TISSUE=Sciatic nerve;
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Neuroblastoma;
MEDLINE=86118662; PubMed=3945311;
                                                                                                                                                                     MEDLINE=92155181; PubMed=1346763;
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                                                                                                                                                                                                                                                                                                                       protein
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                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
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                                                                                                                                                                                                            Neuron
                                                                                                                                                                                                                                                                                   SEQUENCE OF
                                                                                                                                                                                                                                                                                                           Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor-related
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extended
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67; Conser
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Eutheria; Rodentia;
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                                                                                                                                                                                                                   family of protein-tyrosine kinase genes
the vertebrate nervous system.";
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LOCATION: Type I membrane protein
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Pred. No.
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CRC64;
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           A HOMODIMER
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InterPro; IPR004019; YLP_motif.
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PS00109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
brane; Glycoprotein; Multigene family; Receptor; Signal; ase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                          SEQUENCE
                                                                                                                                                                                            EMBL; AE004183; AAF94173.1; -. TIGR; VC1012; -.
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SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor compliance of the tyrosine kinase activity, stimulation synthesis, and cell proliferation.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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000688; Q9B2S2; Q9H2C9; Q9G2X1; Q9H3C9;

121-UL-1986 (Rel. 01, Created)

101-NOV-1997 (Rel. 35, Last sequence update)

15-UN-2002 (Rel. 41, Last annotation update)

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Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray / Liber J., Yarden Y., Libermann T.A., Schlessinger J., Down Lee J., Yarden Y., Libermann T.A., Schlessinger J., Down Lee J., Yarden Y., Libermann T.A., Schlessinger J., Down Lee J., Yarden Y., Waterfield M.D., Seeburg P.H.;
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                        MEDLINE=97078686;
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Ilekis J.V., Stark B.C., Scoccia B.;
"Possible role of variant RNA transcripts
                                                                                                                                                 Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.; "Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cell: Nature 309:418-425(1984).
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MEDLINE=84196372; PubMed=635261;
Lin C.R.; Chen W.S., Kruiger W., Stolarsky L.S.,
Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.
"Expression cloning of human EGF receptor complen
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                               transcript termination in the regulation factor receptor proto-oncogene RNA synthmy. Biol. Chem. 266:1746-1753(1991).
                                                                                                                                                                                                          Waterfield M.D.;
"The human EGF r
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                                                                                                                                                                         "The human EGF receptor gene: structure identification of sequences regulating i Oncogene Res. 1:375-396(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M., Howk R., Givol D., Ullrich A., Schlessinger J.; Howk R. Givol D. Vilrich A., Schlessinger J.; "All autophosphorylation sites of epidermal growth factor (EGF) receptor and HER2/neu are located in their carboxyl-terminal tails. Identification of a novel site in EGF receptor."; J. Biol. Chem. 264:10667-10671(1989).
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"ATP-stimulated interaction
and supercoiled DNA.";
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                                                                                                                                        u. Rev. Biochem. 56:881-914(1987).

FUNCTION: Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation.

FUNCTION: Isoform 2/truncated isoform may act as an antagonist.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
expressed in ovarian cancers.
MISCELLANEOUS: Binding of Egr
dimerization, internalization
induction of the tyrosine kina
                                                   alternative splicing TISSUE SPECIFICITY: 1
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SUBCELLULAR LOCATION:
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d structure of human epidermal growth factor receptor.";
273:11150-11157(1998).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avivi A., Lax I., Ullrich A., Schlessinger J., Giver D., March D., "Comparison of EGF receptor sequences as a guide to study the ligand binding site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00261; FU; 3.
SMART; SM00219; TYTKC; 1.
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tyrosine phosphate.
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SÜBCELLULÄR LÓCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leave the for receptor induction of the tyrosine kinase activity, stimulation of the tyrosine kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AN
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; X78987; CAA55; U03425; AAA17; X59698; CAA42; L06864; AAA53; Z12608; CAA78; Z12608; CAA78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000494; EGFR_L_domain.
IPR000719; Euk_pkinase.
IPR002174; Furin-like.
IPR001245; Tyr_pkinase.
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CAA78249.1;
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ATP-binding; Phosphorylation; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YV30_MYCTU
007035;
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30-MAY-2000 (Rel. 39, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv3130c.
RV3130C OR MT3216 OR MTCY03A2.28 OR MT
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                        This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                             laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                           Peterson J., DeBoy R., Dodson R., Kolonay J.F., Nelson W.C., Umayam Delcher A., Utterback T., Weidman
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinomycetales; Corynebac NCBI_TaxID=1773;
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EMBL; X95986; CAA65230.1;
HSSP; P50162; 1AE1.
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                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical
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                                                                                                                           Eisen J.A., Carpenter L., White O., R., Gwinn M.L., Haft D., Hickey E., mayam L.A., Ermolaeva M.D., Salzberg idman J., Khouri H., Gill J., Mikula
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EMBL; AE007137
TIGR; MT3216;
                                                            "Structural and Included the Additional Cell added domain of mammalian neural cell added to them. 261:3396-3401(1986).
-i- FUNCTION: THIS PROTEIN IS A CELL
                                                                                                                                                                                                                                                                                  SEQUENCE OF 642-725 FROM N.A.
MEDLINE-88283628; PubMed=3396534;
Barbas J.A., Chaix J.C., Steinmetz M.,
"Differential splicing and alternative
distinct NCAM transcripts and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87246524; PubMed=3595563;
Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.
Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
"Isolation and nucleotide sequence of mouse NCAM cDNA that
a Mr 79,000 polypeptide without a membrane-spanning region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCA2_MOUSE STANDARD; PRT; 725 AA P13594; Q61950; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Neural cell adhesion molecule 1, 120 kDa is (NCAM-120).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 20-700 FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-89521563; PubMed-2721486;
Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille "Differential exon usage involving an unusual splicing mechanism generates at least eight types of NCAM cDNA in mouse brain.";
EMBO J. 8:385-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                   SEQUENCE OF 20-36.
MEDLINE=86140120; PubMed=3512556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Structural and immunological characterization
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PF03007; UPF0089;
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-i- SIMILARITY: BELONGS TO THE IMMUNOGLOBULI--i- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LI--i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE
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Pfam: PF00047; ig: 5.
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SMART: SM00060; IGC2; 5.
Cell adhesion; Glycoprotein: T
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Mammalia; Eutheria;
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ALTERNATIVE PRODUCTS: A number of isoforms are produced be alternative splicing.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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IG-LIKE C2-TYPE DOMAIN 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
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HEPARIN-BINDING (POTENTIAL)
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Neural cell adhesion n
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SEQUENCE OF 702-1
STRAIN=C57BL/6; T
MEDLINE=89251563;
                                                                                   SEQUENCE OF 804-1081 FROM N.A. (I
STRAIN-C57BL/6J; TISSUE-Brain;
MEDLINE-88247737; PubMed-24544455;
                                                                                                                             Barbas J.A., Chaix J.C., Steinmetz M., "Differential splicing and alternative distinct NCAM transcripts and proteins EMBO J. 7:625-632(1988).
                                                                                                                                                                                                                                                    Santoni M.-J., Barthe Goridis C., Wille W.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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STRAIN=C57BL/6
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                                        Vopper G., Wille W.; the large isoform of the neural is encoded by an alternatively ids Res. 16:4217-4225(1988).
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                                                                                                                                                                                                                                                                                        Cell adhesion; Glycoprotein; Transmembrane; Repeat; Immunoglobulin domain; Alternative splicing; Signal
                                                                                                                                                                                                                                                                                                              Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 5.
SMART; SM00060; FN3; 2.
SMART; SM00408; IGc2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille "Differential exon usage involving an unusual splicing mechanism generates at least eight types of NCAM cDNA in mouse brain."; EMBO J. 8:385-392(1989).
              CARBOHYD
                                      CARBOHYD
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003961; FN_III.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain of mammalian neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86140120; PubMed=3512556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rougon G., Marshak D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural and
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                                                                                                                                                                                                                                                                                                                                                                                                     BL; X07200; CAA30177.1;

BL; Y00051; F; NOT_ANNOTA

BL; X06328; CAA29641.1;

BL; X07195; CAA30173.1;

BL; X07244; CAA30230.1;

BL; X15051; CAA33150.1;

BL; X15052; CAA33150.1;

BL; X15053; CAA33150.1;

BL; X15052; CAA33151.1;

BL; X15052; CAA33151.1;

BL; X15052; CAA33151.1;

BL; X15052; CAA33151.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 261:3396-3401(1986).
FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane pr
ALTERNATIVE PRODUCTS: 3 isoforms; N-CAM
140 and N-CAM 120 (AC P13594); are produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing.
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                              MGI:97281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long
   ; -; NOT_ANNOTATED_CDS.; CAA29641.1; -. CAA30173.1; -. CAA30230.1; -. CAA33150.1; -. CAA33151.1; -.
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                                                                                                                                    POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

IG-LIKE C2-TYPE DOMAIN 5.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.
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PROBABLE.
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N-LINKED
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                                                                                                                HEPARIN-BINDING HEPARIN-BINDING
                                                                                                      PROBABLE
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(GLCNAC.
(GLCNAC.
(GLCNAC.
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                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                      Signal; Heparin-binding.
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16-OCT-2001 (Rel.
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VARSPLIC
SEQUENCE
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MEDLINE-21332296; PubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Pen

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Pen

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULSO
                                                                                                                          InterPro; IPR001901; SecE.
InterPro; IPR004795; SecE_euk_arch.
TIGRFAMS; TIGR00327; SecE_euk_arch; 1.
PROSITE; PS01067; SECE_SEC610; FALSE_NEG.
PROSITE; Translocation; Transme
Protein transport; Translocation; Transme
TRANSMEM 40 60 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J., "The complete genome of the crenarchaeon Sulfolobus solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
-!- FUNCTION: Involved in protein export (By similarity).
                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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                                                                                                                                                                                                                  EMBL; AE006668; AAK40677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECE OR SSO5663
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                                                                                                                                                                                                                                                                                                                                                               similarity).
SIMILARITY: BELONGS
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QLALTLI
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                                                                                                                                        Translocation; Transmembrane; Complete
                                                                                                                7184 MW;
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MISSING (IN ISOFORM N-CAM 140).
WW; 2C93DCD474CFBCAF CRC64;
                                                                                                                CD51874F424BE9FA
                                                      Mismatches
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NADE_HUMAN
ID NADE_H
AC 000994
AC 000994
DT 01-JUN
DT 15-JUN
DT 15-VUN
DE p75NTR
Associ
GN NGFRAP
OC EURATY
OC MAMMAI
OX NCBLT
RN [1]
RN [1]
RN [1]
RR SEQUEN
RY MEDLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                           RX MEDLINE=98049343; PubMed=9389475;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ktechum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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YI64_ARCFU
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                                                                                                                                 NADE HUMAN STANDARD; PKT; III.....
Q00994;
Q1-UN-1994 (Rel. 29, Created)
Q1-UN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
p75NTR-associated cell death executor (Nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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O28415;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-i- SIMILARITY: Strong, to A.aeolicus AQ_377.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000974; AAB89396.1; -. TIGR; AF1864; -.
MEDLINE=91025550; PubMed=2171551;
                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Archaeog
Archaeoglobaceae; Archaeoglobus.
              TISSUE=Ovary;
                                SEQUENCE FROM N.A
                                                           NCBI_TaxID=9606;
                                                                                                          Homo sapiens (Human)
                                                                                                                         NGFRAP1 OR NADE.
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__arity 100.0%;
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104 AA; 11
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(Rel. 40, Last sequence update)
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1 protein AF1864.
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11845 MW;
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;; Pred. No. 14.
0; Mismatches
                                                                            Craniata; Vertebrata; Catarrhini; Hominidae
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DC80B36CF3F5C153 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be a signaling adaptor molecule involved in p75NTR-mediated apoptosis induced by NGF. May play an important role in the pathogenesis of neurogenetic diseases.
-!- SUBUNIT: Binds to the DEATH domain of p75NTR/NGFR.
-!- TISSUE SPECIFICITY: FOUND IN OVARIAN GRANULOSA CELLS, TESTIS, PROSTATE AND SEMINAL VESICLE TISSUE.
                                                                                                                                                                                                                                 MIM;
                                                                                                                                                                                                                                                            EMBL; M38188; AAA63232.1; --
EMBL; AF187064; AAF75129.1;
EMBL; BC003190; AAH03190.1;
PIR; C35826; C35826.
                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mukai J., Hachiya T., Shoji-Hoshino S., Kimura M.T., Nadano D., Suvanto P., Hanaoka T., Li Y., Irie S., Greene L.A., Sato T.A.; "NADE, a p75NTR-associated cell doath executor, is involved in signal transduction mediated by the common neurotrophin receptor p75NTR.";
                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of three abundant mRNAs from human ovarian
                                                                                          137
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Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Her

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF177761; AAD56009.2; -

InterPro; IPR000494; EGFR_L_domain.

InterPro; IPR002174; Furin-like.

Pfam; PF00757; Furin-like; 1.

Pfam; PF00757; Furin-like; 1.

SMART; SM00261; FU; 1.

SMART; SM00261; FU; 1.
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MEDITINS-99415951; PubMed-10485918;

Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.

"The HER-2/neu receptor tyrosine kinase gene encodes a secautoinhibitor.";
                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999).
[2]
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
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2 (TrEMBLrel. 21,
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-OCT-2001 (TrEMBLrel. 18, Last annotation
Receptor tyrosine kinase EtbB2 (Fragment).
Eukaryota; Metazoa;
           Canis familiaris (Dog)
                     ErbB-2
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Tetens F., Fischer B.;
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Klonisch T., Wolf P.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                  Yu Y., Moshler J.A., Majumdar A.P.N.;
"Cloning of a novel EGFR-related peptide: A putate regulator of EGFR.";
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ date EMBL; AF187818; AAG17037.2;
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR0002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
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Q9ESEO;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
- ''' armal growth factor receptor related protein.
                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00261; FU; 3.

SMART; SM00219; TYFKC; 1.

PROSITE; PS00018; EE_HAND; UNKNOWN_1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500109; PROTEIN_KINASE_TYR; 1.

ATP-binding; Transferase; Tyrosine-protein kinase.

SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;
                                                  SEQUENCE
                                                                                                                                                                       TISSUE=GASTRO-DUODENAL MUCOUS;
                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01030; Recep_L_domain; Pfam; PF02757; YLP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA cloning of erbB-2 from Submitted (OCT-1997) to the I EMBL; AB008451; BAA23127.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                             Receptor
                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P11362;
                                                                                                                                                                                                                                                                                                                                                                                                              292
                                                                                                                                                                                                                                                                                                                                                                                                                                     292
                                                                                                                                                                                                                                                                                                                                                                                                                                                              232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232
                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTF 291
                                                                                                                                                                                                                                                                                                                                                                                                              GASCVT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                     GASCVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00757; Furin-like; 1. PF00069; pkinase; 1.
 Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000719; Euk_pkinase.
IPR002174; Furin-like.
IPR001245; Tyr_pkinase.
IPR004019; YLP_motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002048; EF-hand.
IPR000494; EGFR_L_domain
                                                478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     297
2.1%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1FGK
                                                                                                                                                                                                                                                            (Rat)
                                                                                                                                                                                                                                     Chordata; Rodentia;
                                                  53233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.8%;
Score 9; DB 1; Pred. No. 2.4
0; Mismatches
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66; DB; Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n canine mammary gland
EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                CF873A8376C519E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
           DB 11;
5, 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6; L
. 1.5e-58;
                                                                                                                                                            putative negative
                                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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                        Length 478
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  Indels
                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                     Murinae;
 0;
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                                                                                                                                                                                                                                     Rattus
 Gaps
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us-09-234-208b-2.oli.rspt

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2

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239

QCAAGCTGP

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RESULT
Q9PSH2
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Best Local S
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90836;
Q90836;
01-NOV-1996
                                                                                                                                                                                      O9PSH2 PRELIMINARY; PRT; 599 AA.
O9PSH2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Elidermal growth factor receptor (Fragment).
Pfam;
                                                        "A complete description of the
                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flickinger T.W., Maihle N.J., Kung
"An alternatively processed mRNA fi
soluble, truncated form of the rece
         Pfam; PF00757;
                     implication in oncogenic activation oncogene 8:2939-2948(1993). Oncogene 8:2939-29484, EGFR_L_domain InterPro; IPR0002174; Furin-like.
                                                                             Callaghan T., Antczak M., Kung H.J.;
                                                                                                 SEQUENCE FROM N.A. MEDLINE-94020816;
                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dependent transformation.";
Mol. Cell. Biol. 12:883-893(1992).
EMBL; M77637; AAA48759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-ERBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF/TGF-alpha receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92123214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                       245
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                                                                                                                                                                                                                                                                                                                            QCAAGCTGP 247
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 PF01030;
                                                                                                                                                                                                                                                                                                                                                  Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               527
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                              ΑĄ,
Recep_L_domain; 2.
           Furin-like;
                                                                                                                                                                                                                                                                                                                                                                                  28
527
58353 }
                                                                                                  PubMed=8414496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1732751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                             2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor.
                                                     activation
                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                     Flickinger T., Raines M.,
                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                             Score 9;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                             EGF/TGF-ALPHA RECEPTOR
764564ABCC095298 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                     EGF-receptor exa
ation and domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA from the avian or receptor that can
                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.-J.;
                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527
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o. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                               exon
                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                      Length 527;
                                                      evolution
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n block
                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                      structure:
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                      Myers
                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene encodes
ligand-
                                                                                                                                                      Phasianinae
                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 8
Q9WVF5
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Q9ERV6
  В
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                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                EMBL; AF275366; AAG28046.1; -...
EMBL; AF275365; AAG28046.1; -...
EMBL; AF275365; AAG28046.1; JO1
MGD; MGI:95294; Egfr.
InterPro; IPR000345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                            09WVF5;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Epidermal growth factor r
                                                                                                                                                                                                                                                                     Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C3H/LOI, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                              EGFR
                                                                                                                                                                                                                                                                                                    InterPro; IPR000345; Cytc_heme_bind
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21, Epidermal growth factor rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ERV6;
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00261; FU; SEQUENCE 599 AA;
                                                                                                                        Q9WVF5
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative genomic sequence analysis and mouse alternative Egfr transcripts encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                Mus musculus (Mouse)
                                                       isoform
                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGFR.
                                                                                                                                                                              235 QCAAGCTGP 243
                                                                                                                                                                                                   239 QCAAGCTGP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 QCAAGCTGP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCAAGCTGP
                                                                                                                                                                                                                          Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
9; Conserv
                                                                                                                                                                                                                                                                                          PS00190;
                                                                                                                                                                                                                                                                      643 AA;
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                                          CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 3.
66363 MW;
            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                     71476 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,1%;
                                                                                                                                                                                                                                   2.1%;
                                                                         12, Created)
12, Last sequence 21, Last annotation
                                                               12, Last sequence update)
21, Last annotation update)
receptor (Epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21, Last annotation update) receptor isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last
Last
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
                                                                                                                                                                                                                                   Score 9;
                                                                                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; DB 1
Pred. No. 2.9
0; Mismatches
          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                     DEF22002C84911B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEAB46D293D991BD CRC64;
                                                                                                                                                                                                                         red. No. 3. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                        655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643
                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13;
. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                         truncated receptor
                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                              Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                   factor receptor
                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
           Murinae;
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                         Gaps
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Q9QX70
ID Q1
AC Q1
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                                                                                                                                                                                                Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).

EMBL; AF124513; AAD44149.1: -
EMBL; AF275366; AAG28047.1; JOINED.
EMBL; AF275365; AAG28047.1; JOINED.
EMBL; AK004944; BAB23688.1; -
EMBL; AK004883; BAB23641.1; -
EMBL; AK004883; BAB23662.1; -
EMBL; AK004911; BAB23662.1; -
MGD; MGI:95294; EGFR_L_domain.
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR000494; Furin-like.
Q9QX70
Q9QX70;
                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-LIVER;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lamp
Balasubramaniam S., Crossley T.O., Magnuson T.R., Jame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wynshaw-Boris A
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse alternative
isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Alternative Transcripts from the Human and Carboxy-Terminal Truncated Receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lampland A.L., Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell C.,
Lampland A.L., Balasubramaniam S., Crossley T.O., Magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative genomic sequence analysis and isolation mouse alternative Egfr transcripts encoding truncated
                                                                                                                       235
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                                                                                                                                                                                                                                                                                                                                              PF00757;
                                                                                                                       QCAAGCTGP
                                                                                                                                                           QCAAGCTGP
                                                                                                                                                                                                  Similarity
9; Conserv
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                        PRELIMINARY;
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                                                                                                                       243
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                                                                                                                                                                                                                                                                                                                       Recep_L_domain;
; FU; 3.
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                                                                                                                                                                                                                                                                                  72906 MW;
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5. 3.1;
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                                                                                                                                                                                                                                       Length 655;
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Q9EP98
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JT 01-UN-2002 (TrEMBLrel. 21
DT 01-UN-2002 (TrEMBLrel. 21
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Best Local S
Matches 9
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Pfam: PF00069; pkinase; 1.
Pfam: PF001030; Recep_L_domain; 2.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
PRODOM; PD0000261; FU; 3.
SMART; SM00261; TYFKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guttridge K., Dawson T.L., I Submitted (NOV-1999) to the
STRAIN=C3H/101, 129/SVJ, AND 129/SVEVTAC; Reiter J.L., Threadgill D.W., Eley G.D.,
                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding;
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M37394; AAF14008.1; HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1991) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                           SEQUENCE FROM
                                                                               NCBI_TaxID=10090;
                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A truncated, secreted form of the epidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                239 QCAAGCTGP
                                                                                                                                                                                                                                                                                                                                                                                        235 QCAAGCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000494;
IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%;
milarity 100.0%;
Conservative 0;
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                                                                                                                                         (Mouse)
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oa; Chordata;
ia; Rodentia;
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                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134891 MW;
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                                                                                                                                                                                 16, Creat
16, Last
21, Last
receptor
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e EMBL/GenBank/DDBJ
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0; Mismatches
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                                                                                                                                                                                                                                               Created)
                                                                                                 Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                   annotation isoform 1.
                                                                                                                                                                                                                        sequence update)
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5.4;
                                                                                                                        Vertebrata;
    Strunk
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                                                                                                      Muridae;
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    Χ.E.,
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; Murinae; Rat
                                                                                                      Euteleostomi;
; Murinae; Mus
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    Danielsen
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    А. J.,
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Best Local
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InterPro; IPRO02174; Furin-like.
InterPro; IPRO02290; Ser_thr_pkinase.
InterPro; IPRO01245; Tyr_pkinase.
InterPro; IPRO01245; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; 
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                                                     SEQUENCE FROM N.A.
MEDLINE=91061737; PubMed=2123292;
Suen T.C., Hung M.C.;
Multiple_cis- and trans-acting e
      meu
Mol.
                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mamumalia; Eutheria; Rodentia;
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MGD; MGI:95294; Egfr.
InterPro; IPR000345; CytC_heme_bind
InterPro; IPR000494; EGFR_L_domain.
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EMBL; AF275366; AAG28045
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                                                                                                                                                                                                              NCBI_TaxID=10116;
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Sciurognathi;
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uson T.R., James
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chi; Muridae; Murinae; Rat
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01-MAY-2000 (TrEMBLrel 13,
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01-MAY-2000 (TrEMBLrel 13,
SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE=OVARY;
ESPEY L.L., YOShioka S., Russell D., Usper Varian S., Okamura H., Richards J.S.;
"Characterization of Ovarian Carbonyl Ovulation in the Gonadotropin-Primed 1
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A STRAIN-WISTAR; TIS
                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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SEQUENCE FROM N.A.
MEDLINE=91172172;
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                                                                                                   Rattus norvegicus
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EMBL; M61004; AAA41686.1; -
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Q9N6W6
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Matches 8; Conserv
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SEQUENCE FROM N.A.
STRAIN-WISTER; TISSUB-OVARY;
MEDLINE-97167735; PubMed-9015353;
Aoki H., Okada T., Mizutani T., Numata Y., Minegishi T.,
"Identification of two closely related genes, inducible a
noninducible carbonyl reductases in the rat ovary.";
                                                                                                                                                                                                                                                                                                                                                                                                                               008558;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel.) Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0012370; Dhyd\HLHm-gamma.
InterPro; IFR001092; HLH_basic.
InterPro; IFR001650; Orange.
pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00351; ORANGE; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Spatially restricted factors co-operate with Notch in the regulation of Enhancer of Split genes.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ276313; CAB77019.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Cooper M.T.D., Tyler D.M., Furriols M.,
Bray S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9N6W6;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF181956; AAF03395.1; - NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                   Inducible carbonyl reductase.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   008558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea; Dro
NCBI_TaxID=7224;
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HLHM-GAMMA OR E.
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                                                                                                                                                                                                                                      NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia;
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| SVPISPVS 166
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8; Conserv
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                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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o. 12;
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o. 4.1;
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                                                   and
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PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                                                                                                                                                                          (SDR) FAMILY.
EMBL; D89069; BAA19007.1;
HSSP; P50162; 1AE1.
                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 230:518-523(1997).
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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SEQUENCE 277 AA;
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US-09-344-195-4
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US-08-444-4178-68
US-08-448-348-68
US-08-468-5458-68
US-08-468-6808-68
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US-08-468-786-2
US-08-468-786-2
US-08-468-783-3
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                                                                                                                       Query Match
Best Local Similarity
Matches 419; Conserv
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                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 206 628-7699 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                            1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: polypeptide
SEQUENCE DESCRIPTION: SEQ I
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MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
ADDRESSEE: Teourth Avenue, 2600 Century Square
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/630,155
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORD CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Doherty, Joni Kristin and Gail M. Clinton TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
                                      \tt MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                              LENGTH: 419
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Davison, Barry L. REGISTRATION NUMBER: 47,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Washington COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 206 628-7621
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                                                                                                                    100.0%; Score 419; Inilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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RESULT 2
US-09-146-283-4
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                Query Match
Best Local Similarity
 Matches
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7638
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Laus, Reiner
APPLICANY: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunos
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acid
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ADDRESSEE: Dehlinger & Associates
                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
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                                                                                  INDIVIDUAL ISOLATE:
                                                                                                    ORGANISM:
                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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amino acid
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 Conservative
                                                                                                    homo sapiens
                                                                                                                                                                        linear
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)N: 536
                81.1%; Score 340; I
100.0%; Pred. No. 9
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                                                                                  GM-CSF-Her-2 fusion protein; Fig.
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Mismatches
                                DB 2;
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Query Match
Best Local Similarity
Matches 340; Conserv
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                                                                                                                                                                                                                                     TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                  MOLECULE TYPE: pi
HYPOTHETICAL: NO
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wu, HOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                               ORGANISM: homo sapiens INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein;
                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                      TELEPHONE: 050-324-0960
                                                                                                                                                                                                                                                                                                                  NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/579,823A FILING DATE: 03-DEC-1998
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                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruegg, Curtis L.
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                                                                                                                                                                     linear
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                                                                                                                                                  protein
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81.1%; Score 340; DB 3; L
100.0%; Pred. No. 9.7e-317;
tive 0; Mismatches 0;
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RESULT 4
US-09-344-195-4
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Patent No. 6210662
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
                                                                                                                                                      TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                    APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.
TELEPHONE: 650-324-0880
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FILING DATE: 24-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite
ORGANISM: homo sapiens INDIVIDUAL ISOLATE: GM-SEQUENCE DESCRIPTION: SEQ II
                                                 HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Immunostimulatory Compositions NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNYLSTDYGSCTLYCPLHNQEVTAEDGTQRCEKCSKPCAR 340
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                                                                                                                     TYPE: amino acids
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ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruegg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hongyu
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   GM-CSF-Her-2 fusion protein;
Q ID NO: 4:
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               Fig.
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RESULT 5
US-08-467-083-68
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            ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-631
TELEFAX: (206) 682-6031
TELEFAX: 723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 68.
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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Best Local S
                                                                                                                                                                                                                                                                                     COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC CONS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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APPLICANT: Cheever, Marti
APPLICANT: Disis, Mary L.
                                                                                                                                                                                                                         APPLICATION NUMBER: (FILING DATE: 06-JUN-CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 CONTY: Seattle STATE: Washing
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                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995
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LENGTH:
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06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNE REACTIVITY TO HER-2/NEU PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES HER-2/NEU ONCOGENE IS ASSOCIATED
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9.7e-317;
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US-08-414-417B-68
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                                                                                                              APPLICATION NUMBER: US/08/414,417B
APPLICATION: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 320010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 340; Conservative
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                                                                                     TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
CITY: Se
STATE: W
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                                                  1255 amino acids
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100.0%;
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ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-CCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 11-NOV-1993
CLASSIFICATION STANDARD STANDARD STANDARD NUMBER: US 08/150,704
FILING DATE: 11-NOV-1993
CLASSIFICATION. 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08484438 Patent No. 5811098 Patent No. 5811098 5780031 GENERAL INFORMATION:
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                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE NUMBER OF SEQUENCES: 42
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STREET: 1155 Ave.
CITY: New York
STATE: New York
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                                                                                           APPLICATION NUMBER: FILING DATE: 24-NOV
                                                                                                                                                      CLASSIFICATION:
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                 REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 5624-230
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1155 Avenue of the Americas
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                               S. Leslie
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                                                                                                               US 07/981,165
               18,872
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TELECOMMUNICATION INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 68, Applia Patent No. 5846538
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 32,629
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Best Local :
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TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
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MOLECULE TYPE:
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LENGTH: 1255 amino acids
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STREET: 63
CITY: Seat
STATE: Was
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REFERENCE/DOCKET
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                                                                                                                                                                                                              98104-7092
                                                                                                                                                                                                                                                             Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08486348A
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100.0%;
 NUMBER:
                                                                                                                                                                                                                                                                       Center, 701
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920010.448C6
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                                                                                                                                                                                                                                                                          Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Mary L.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 32,0010.448C7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08625101 Patent No. 5869445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Co
CITY: Seattle
STATE: Washing:
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                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                                                                                                                                                                                                                                                Washington
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Pred. No. 1.5e-316;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          701 Fifth Avenue
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TELEFAX: (206) 682-60: INFORMATION FOR SEQ ID NO:

(206) 682-6031

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US-08-468-545B-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5876712 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 68,
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Best Local Similarity
TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
               NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Sharkey, Richard G
                                                                                                                                                                                                                                                                                                                         STREET: 6300 COUNTRY: Seattle STATE: Washing COUNTRY: US
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                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-JUN
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                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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                                                                                                                                                                                                                                                                                                                                            Washington
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                                                                                                                                                                                                                                                                                                                                                                                  6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                             NUMBER: US/08/468,545B
06-JUN-1995
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                                                                       920010.448C5
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RESULT 11
US-08-356-786-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 340;
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Best Local Similarity
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,96;
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CAPPLICANT: CAPPLICANT: FAPPLICANT:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Excha
CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ring, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huston, James S.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                  CRP-053
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Length 1255;

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RESULT 12
US-08-466-680B-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 68, Application US/08466680B Patent No. 6075122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Cheever, Marti
APPLICANT: Disis, Mary L.
                  TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
                                                    REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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                                                                                  NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 920010.448C4
                                                                                                                                                                FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                98104-7092
                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                    6300 Columbia Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheever, Martin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                     682-6031
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US-08-422-108-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1,
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                                                                                                   CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/355

FILING DATE: 13-DEC-1994

PRIOR APPLICATION NUMBER: 08/048

APPLICATION NUMBER: 08/048

FILING DATE: 15-APR-1993

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
FILING DATE: 14-Apr-1995
                                               APPLICATION NUMBER: 07/3
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hudziak, Robert M. APPLICANT: Shepard, H. Michae APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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ZIP: 94080
               NAME: Lee, Wendy M
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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South San Francisco
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GY: linear
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ilarity 100.0%;
Conservative (
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554C2D2
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TELECOMMUNICATION INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                GENERAL GENERAL GENERAL APPLICANT: Shepard, H. Michael APPLICANT: Shepard, H. Michael APPLICANT: Ullrich, Axel TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-422-734-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08422734
Patent No. 6333169
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
TYPE: Amino Acid
                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422108
FILING DATE: 14-Apr-1995
APPLICATION NUMBER: 08/355460
                 FILING DATE: 13-DEC-PRIOR APPLICATION DATA:
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                                                                                                                                                   FILING DATE:
                                                                                                                                                                   APPLICATION NUMBER:
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08/048346
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Patent No. 5783404
GENERAL INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HE NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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LENGTH: 624 amino acids
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                                                                     CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                            STREET: 1840 Dehavilland
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                                APPLICATION NUMBER: US/08/421,356 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                 CLASSIFICATION:
                                                                                                                                                                               ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 76.1%; Score 319; DB 4; Lucal Similarity 100.0%; Pred. No. 9.4e-297; es 319; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
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                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee, Wendy M
                                                                                                                                                                                                                                                                                                                             Koski, Raymond A.
                                                                                                                                                                                                                                                                      Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1993
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-327
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-421-356-3

QUETY MATCH
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
MATCHES 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
MATCHES 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0

96 LORLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLI 155
MATCHES 96; CONSERVALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLI 61

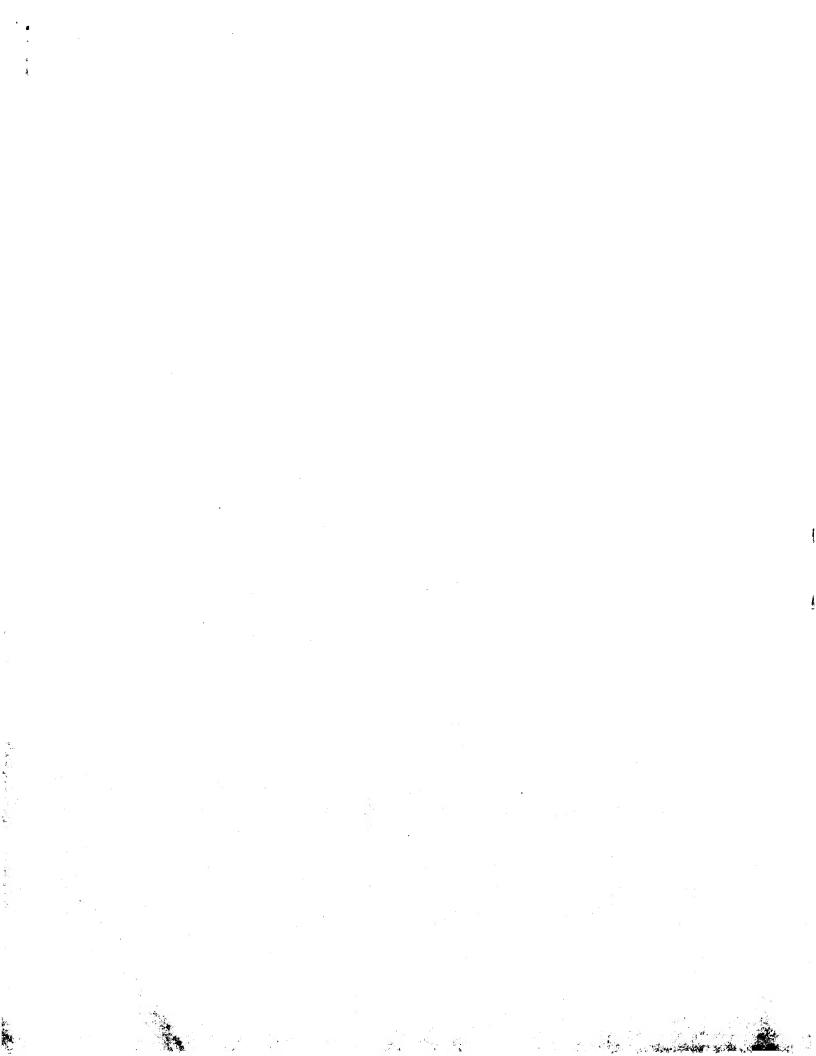
QY 96 LORLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLI 61

QY 156 QRNPOLCYQDTILWKDIFHKNNQLALTLIDTNRSRA 191

QY 156 QRNPOLCYQDTILWKDIFHKNNQLALTLIDTNRSRA 97

Search completed: March 4, 2003, 12:48:29

Job time: 35.6546 secs
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Copyright

GenCore version (c) 1993 - 2003

5.1.3 Compugen Ltd

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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                             Score
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1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/PCTUS.PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/PCTUS.PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

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		Sequence 204, App	Sequence 12896, A	Sequence 13700, A	Sequence 13383, A	Sequence 18, Appl	_	٠.	•	-	•	22,	Sequence 21, Appl		Sequence 17, Appl		-	31,		Sequence 12, Appl	Sequence 20, Appl		Sequence 19, Appl	Sequence 14, Appl	Sequence 118, App

ALIGNMENTS

US-09-921-161-1 RESULT 1

Sequence 1, Application US/09921161 Patent No. US20020090662A1

GENERAL INFORMATION:
APPLICANT: Ralph, Peter
TITLE OF INVENTION: ANALYTICAL METHOD
FILE REFERENCE: GENENT.066A

PRIOR APPLICATION NUMBER: 60/225,433
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 1

SOFTWARE: FastSEQ for Windows Version

CURRENT APPLICATION NUMBER: US/09/921,161 CURRENT FILING DATE: 2001-08-01

2001-08-01

SEQ ID NO 1 LENGTH: 645

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Best Local Similarity
Matches 340; Conserv
241 AAGĆTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                   LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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Conservative
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                                                                                                                                                                                    RESULT 3
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                                                                                                 Sequence 7, Application US/09854356 Patent No. US20020177567A1 GENERAL INFORMATION:
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APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKilne Beecham Biologicals
TITLE OF INVENTION: HER-2/neu Fusion Protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: Smithkline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.1
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TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 4
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US-09-854-356-7
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                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 6
LENGTH: 919
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                            APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: Smithkline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
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CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
OTHER INFORMATION: OTHER INFORMATION:
                                                       ORGANISM: Artificial Sequence
                                                                             TYPE: PRT
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                                      FEATURE:
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Description of Artificial Sequence:fusion protein of ECD and PD of human HER-2/neu
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US-09-769-508-2
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09769508 Patent No. US20020155527A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                          Query Match 81.1%; Score 340; DB 9; Louis Local Similarity 100.0%; Pred. No. 1.7e-302; Matches 340; Conservative 0; Mismatches 0;
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Best Local (
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APPLICANT: MONAHAN, JOHN J.
APPLICANT: LANGTON, BEATRICE CLAUDIA
APPLICANT: HANCOCK, MIRIAM E.C.
APPLICANT: CHAO, LORRINE A.
APPLICANT: BLUFORD, PETER
TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN:
FILE REFERENCE: BEBIO-111-C1
                                                                                                                                                                                                                                                                                                                                           LENGTH: 1255
TYPE: PRT
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; LOCATION: (990)..(1048)
; OTHER INFORMATION: fragment of the phosphorylation domain,
OTHER INFORMATION: portion (delta PD)
US-09-854-356-1
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US-09-854-356-1
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CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.1
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Best Local
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LENGTH: 1255
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APPLICANT: Gheysen, Dirk
APPLICANT: Gorbysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals
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LOCATION: (990)..(1255)
OTHER INFORMATION: phosphorylation
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OTHER INFORMATION: extracellular domain (ECD)
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AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                                    DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
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CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1255
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                                                                                                                                   Sequence 6, Application US/09441411
Publication No. US20030008342A1
GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
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APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND
TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.544
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100.0%;
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Best Local S
Matches 340
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SEQ ID NO 9
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LENGTH: 1255
                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                              Matches 340;
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CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR APPLICATION NUMBER: 09/602,530
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows
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TYPE: PRT
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 1.7e-302;
tive 0; Mismatches 0;
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0; Mismatches 0;
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TITLE OF INVENTION: HER 2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENENT 034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILLING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILLING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1255
TYPE: PAT
CORGANISM: Homo sapiens
US-09-811-115-3
         US-09-821-883-5
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Sequence 5, Application US/09821883 Patent No. US20020061310A1
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Best Local Similarity
Matches 340; Conserv
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APPLICANT: Schwall, Ralph
APPLICANT: King, Kathleen
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Query Match

Best Local Similarity

69.7%; 100.0%;

Score 292; Pred. No.

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US-09-821-883-1
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                                                                                      PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 1
LENGTH: 555
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APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
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                                                                                                                                                                                                 TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30 CURRENT APPLICATION NUMBER: US/09/821,883 CURRENT FILING DATE: 2001-03-30 CURRENT FILING DATE: 2001-03-30
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TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
CURRENT FILING DATE: 2001-03-30
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SOFTWARE: FastSEQ for Windows Version 4.0
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               OTHER INFORMATION: HER500 construct
                                                   ORGANISM: Artificial Sequence
                                                                      TYPE: PRT
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Qy DЬ 20 Db Qy DЬ Q DЬ

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RESULT 13
US-09-821-883-3
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PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 3
LENGTH: 564
TYPE: PRT
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Best Local
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APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
CURRENT FILING DATE: 2001-03-30
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US-09-821-883-4
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                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods :
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
                                                                                             NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Best Local :
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APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods:
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09821883 Patent No. US20020061310A1
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
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TYPE: PRT
                              TYPE: PRT ORGANISM: Artificial Sequence
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  OTHER INFORMATION: HER500*-rGM-CSF
                      FEATURE:
                                                                          LENGTH: 697
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                                                      139 ELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPM 198
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